

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 04:53:20 ; Search time 8937.89 Seconds
(without alignments)
1124.566 Million cell updates/sec

Title: US-09-806-197-1

Perfect score: 2052

Sequence: 1 catgtgtgcctcacagcagcaca.....gcatacatcttaataatc 2052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Genbankl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_lm:*
5: gb_ov:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description |
|------------|--------|-------------|--------|------------|----------------------|
| 1 | 2052 | 100.0 | 2052 | 6 E40087 | E40087 Plant promo |
| 2 | 2048.8 | 99.8 | 2052 | 6 E40093 | E40093 Plant promo |
| 3 | 2038 | 99.3 | 2056 | 6 E40091 | E40091 Plant promo |
| 4 | 2034 | 99.1 | 2048 | 6 E40090 | E40090 Plant promo |
| 5 | 2032.4 | 99.0 | 2048 | 6 E40089 | E40089 Plant promo |
| 6 | 241.2 | 11.8 | 2042 | 6 AR076817 | AR076817 Sequence |
| 7 | 241.2 | 11.8 | 2042 | 6 E15125 | E15125 Promoter. 7 |
| 8 | 196.6 | 9.6 | 247 | 6 AR076816 | AR076816 Sequence |
| 9 | 196.6 | 9.6 | 247 | 6 E15124 | E15124 Promoter. 7 |
| 10 | 195.6 | 9.5 | 246 | 6 AR146852 | AR146852 Sequence |
| 11 | 195.6 | 9.5 | 246 | 6 E55065 | E55065 Plant promo |
| 12 | 174 | 8.5 | 8005 | 6 DCA18706 | DCA18706 Daucus caro |
| 13 | 162.4 | 7.9 | 2831 | 6 BD188672 | BD188672 Promotor |
| 14 | 162.4 | 7.9 | 2865 | 6 BD188674 | BD188674 Promotor |
| 15 | 162.4 | 7.9 | 4886 | 8 DARC852 | D16355 Carrot gchs |
| 16 | 119 | 5.8 | 140 | 6 AR146856 | AR146856 Sequence |
| 17 | 119 | 5.8 | 140 | 6 AR146857 | AR146857 Sequence |
| 18 | 119 | 5.8 | 140 | 6 E55069 | E55069 Plant promo |
| 19 | 119 | 5.8 | 140 | 6 E55070 | E55070 Plant promo |

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| c | 20 | 106.6 | 5.2 | 250029 | 3 | AE014839 | AE014839 Plasmodiu |
| c | 21 | 103.6 | 5.0 | 172816 | 9 | AC093899 | AC093899 Homo sapi |
| c | 22 | 101.8 | 5.0 | 258658 | 3 | AE014832 | AE014832 Plasmodiu |
| c | 23 | 100.4 | 4.9 | 348174 | 3 | CR382399 | CR382399 Plasmodiu |
| c | 24 | 99.4 | 4.8 | 8056 | 6 | AX599046 | AX599046 Sequence |
| c | 25 | 99.2 | 4.8 | 205130 | 2 | AC105425 | AC105425 Homo sapi |
| c | 26 | 97 | 4.7 | 14867 | 3 | AE001398 | AE001398 Plasmodiu |
| c | 27 | 96.6 | 4.7 | 67970 | 3 | PFMALP3 | AL031746 Plasmodiu |
| c | 28 | 96.4 | 4.7 | 4601 | 3 | DMU11584 | U11584 Drosophila |
| c | 29 | 96.4 | 4.7 | 19517 | 3 | DMU37541 | U37541 Drosophila |
| c | 30 | 95.8 | 4.7 | 64394 | 3 | AL928596 | AL928596 Human DNA |
| c | 31 | 95.2 | 4.6 | 313050 | 3 | PFPA929352 | AL929352 Plasmodiu |
| c | 32 | 93.8 | 4.6 | 143331 | 9 | AC091214 | AC091214 Homo sapi |
| c | 33 | 93 | 4.5 | 349980 | 6 | AX344555 | AX344555 Sequence |
| c | 34 | 92.6 | 4.5 | 180629 | 2 | CR388025 | CR388025 Danio rer |
| c | 35 | 92.6 | 4.5 | 349751 | 3 | PFMAL43 | AL035476 Plasmodiu |
| c | 36 | 92.4 | 4.5 | 261771 | 2 | CR356223 | CR356223 Danio rer |
| c | 37 | 91.8 | 4.5 | 8056 | 6 | AX598900 | AX598900 Sequence |
| c | 38 | 91.6 | 4.5 | 8056 | 6 | AX599046 | AX599046 Sequence |
| c | 39 | 91 | 4.4 | 21153 | 8 | YSCWTCG13 | L36897 Saccharomyc |
| c | 40 | 91 | 4.4 | 118642 | 9 | AC126283 | AC126283 Homo sapi |
| c | 41 | 91 | 4.4 | 178427 | 2 | CR392006 | CR392006 Danio rer |
| c | 42 | 90.8 | 4.4 | 86826 | 3 | PFMAL3P5 | AL034556 Plasmodiu |
| c | 43 | 90.6 | 4.4 | 155106 | 9 | AC104069 | AC104069 Homo sapi |
| c | 44 | 90.6 | 4.4 | 178670 | 9 | AC104073 | AC104073 Homo sapi |
| c | 45 | 90.6 | 4.4 | 206038 | 2 | CR847802 | CR847802 Danio rer |

ALIGNMENTS

RESULT 1
E40087
LOCUS E40087 2052 bp DNA linear PAT 31-JAN-2002
DEFINITION Plant promoter and terminator.
ACCESSION E40087
VERSION E40087.1 GI:18627203
KEYWORDS JP 2000166577-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2052)
AUTHORS Nishikawa,S. and Oeda,K.
TITLE Plant promoter and terminator
JOURNAL Patent: JP 2000166577-A 1 20-JUN-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
PN JP 2000166577-A/1
PD 20-JUN-2000
PF 01-OCT-1999 JP 1999281475
PR
PI SATOMI NISHIKAWA,KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,C12N5/10//C12N5/10,C12R1:91, PC
C12N15/00,
PC C12N5/00,C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

Query Match 100.0%; Score 2052; DB 6; Length 2052;
Best local similarity 100.0%; Pred. No. 4.4e-310;
Matches 2052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTCTTCTCTTTGACCTGTTGTAATAAGATGAAATATTTTAAAAAGCTGGAA 120
DB 61 CTTCTTCTCTTTGACCTGTTGTAATAAGATGAAATATTTTAAAAAGCTGGAA 120
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DB 361 CCGTCTTCCAAAGATAATATTTTAAATTTTGAAGCTCCCTTTAACCAATTCGATGC 420
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DB 1621 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
QY 1681 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
DB 1681 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
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QY 1921 AACACCTCAACCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 AACACCTCAACCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 CACATCAATCTTAAACCAACCTTAAATGATGATGATGATGATGATGATGATGATGAT 2040
DB 1981 CACATCAATCTTAAACCAACCTTAAATGATGATGATGATGATGATGATGATGATGAT 2040
QY 2041 ATTCTAAATTAAT 2052
DB 2041 ATTCTAAATTAAT 2052

RESULT 2
E40093
LOCUS
DEFINITION Plant promoter and terminator.
ACCESSION E40093
VERSION E40093.1 GI:18627209
KEYWORDS UP 2000166577-A/7.
SOURCE
ORGANISM unidentified

unclassified.
1 (bases 1 to 2052)
AUTHORS Nishikawa,S. and Oeda,K.
TITLE Plant promoter and terminator
JOURNAL Patent: JP 200016577-A 7 20-JUN-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
PN JP 200016577-A/7
PD 20-JUN-2000
PP 01-OCT-1999 JP 1999281475
PR
PI SATOMI NISHIKAWA,KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,C12N5/10//C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT promoter (1)..(2052).
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ORIGIN
Query Match 99.8%; Score 2048.8; DB 6; Length 2052;
Best Local Similarity 99.9%; Pred.No.1,4e-309;
Matches 2050; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CATGTGCGCTTACAGACATAGAGGCGCTGTTGGTTGAGAGAGCAGAACTGCTCTGA 60
DB 1 CATGTGCGCTTACAGACATAGAGGCGCTGTTGGTTGAGAGAGCAGAACTGCTCTGA 60
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Qy 2041 ATTCTAATATC 2052
Db 2041 ATTCTAATATC 2052
RESULT 3
E40091
LOCUS E40091 2056 bp DNA linear PAT 31-JAN-2002
DEFINITION Plant promoter and terminator.
ACCESSION E40091
VERSION E40091.1 GI:18627207
KEYWORDS JP 2000166577-A/5.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2056)
AUTHORS Nishikawa,S. and Oeda,K.
TITLE Plant promoter and terminator
JOURNAL Patent: JP 2000166577-A 5 20-JUN-2000;
COMMENT OS Daucus carota L.
PN JP 2000166577-A/5
PD 20-JUN-2000
PR 01-OCT-1999 JP 1999281475
PI SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,C12N5/10//C12N5/10,C12R1:91), PC
CC C12N5/00,C12N5/00,C12R1:91)
FH
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Location/Qualifiers
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ORIGIN
Query Match 99.3%; Score 2038; DB 6; Length 2056;
Best local Similarity 99.8%; Pred. No. 6.7e-308;
Matches 2052; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 CATGTGTGCCCTTACGACATATGAGGCTGTTGGTTAGAGAGACAGAGCTGCTTGA 60
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Db 841 AAAAAGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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Db 901 TAAAGTATCTAAGACATAGAAATTTAGTAAAGTAAACCTTTTCAAGATTTATA 960
Qy 961 TTAAGGAAATCAATTTTAAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
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Db 1201 AAGAGGAAAAAAGTGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1260

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| QY | 781 | ATTAGAGCTATTAACTTAAGTACTTAATAATAAGAGGTTAGTAAACAGAAAGCAGTAA | 840 |
| Db | 777 | ATTAGAGCTATTAACTTAAGTACTTAATAATAAGAGAGGTTAGTAAACAGAAAGCAGTAA | 836 |
| QY | 841 | AAAACAGAGGCTTGCTGCTGTGTGTTTGAAGTTGGTGTGAGCCATTTCTTTAAAGTATG | 900 |
| Db | 837 | AAAACAGAGGCTTGCTGCTGTGTGTTTGAAGTTGGTGTGAGCCATTTCTTTAAAGTATG | 896 |
| QY | 901 | TAAACTGATCTTAAGCACTAGAAATTTTAGTACAGGTTAAACCTTTTACAGAATTTAT | 960 |
| Db | 897 | TAAACTGATCTTAAGCACTAGAAATTTTAGTACAGGTTAAACCTTTTACAGAATTTAT | 956 |
| QY | 961 | TTTAAACGAAAATCATTTTATATACATGCTCTCGGGCTGCAATTAATAAGGATCATTTAC | 1021 |
| Db | 957 | TTTAAACGAAAATCATTTTATATACATGCTCTCGGGCTGCAATTAATAAGGATCATTTAC | 1011 |
| QY | 1021 | TGATCATCCATTAAACCTTGTTAAACAAATTCATGAGATTAATAATCTTATCAATGAA | 1081 |
| Db | 1017 | TGATCATCCATTAAACCTTGTTAAACAAATTCATGAGATTAATAATCTTATCAATGAA | 1076 |
| QY | 1081 | AAGAAGCAATATGCTCTTTGAAAAACAAATAGCTACTCCCTCGCTCCCTTGAAATGT | 1144 |
| Db | 1077 | AAGAAGCAATATGCTCTTTGAAAAACAAATAGCTACTCCCTCGCTCCCTTGAAATGT | 1136 |
| QY | 1141 | ATCAATATGATTGAGACACGAGACTAAGAAAAATGTATTAAGTATATAGATTAATAAG | 1201 |
| Db | 1137 | ATCAATATGATTGAGACACGAGACTAAGAAAAATGTATTAAGTATATAGATTAATAAG | 1196 |
| QY | 1201 | AAAAGAGAAAGAAAGTGCGTTAAAGTACCGGACCCCAATATATATATGATTAAGTTAG | 1260 |
| Db | 1197 | AAAAGAGAGAAAGAAAGTGCGTTAAAGTACCGGACCCCAATATATATATGATTAAGTTAG | 1256 |
| QY | 1261 | AAAAGTATGTTGAAGAATGATGGGTGGGTGGGATTTTATATATTAATAAATTTATCTATTTG | 1320 |
| Db | 1257 | AAAAGTATGTTGAAGAATGATGGGTGGGTGGGATTTTATATATTAATAAATTTATCTATTTG | 1316 |
| QY | 1321 | AGAAAGTTTGAAGATGTATAGAAATTAAGTGGGACATCCATAAAGAAAGTATAGAAAT | 1380 |
| Db | 1317 | AGAAAGTTTGAAGATGTATAGAAATTAAGTGGGACATCCATAAAGAAAGTATAGAAAT | 1376 |
| QY | 1381 | TAAATGGGACAGAGGAGTATATACCTTTATGATATATATAATTTTGTATTTGATTTTCA | 1440 |
| Db | 1377 | TAAATGGGACAGAGGAGTATATACCTTTATGATATATATAATTTTGTATTTGATTTTCA | 1436 |
| QY | 1441 | TAAATTTAATAATCTATGTTATATATATATTAATAAATAATAATCTATATTAAT | 1500 |
| Db | 1437 | TAAATTTAATAATCTATGTTATATATATATTAATAAATAATAATCTATATTAAT | 1496 |
| QY | 1501 | CTGATATAGTCGATTAACCGCTTTTATTAATTTTAACAATCTGAGTAAATATATATATCAG | 1560 |
| Db | 1497 | CTGATATAGTCGATTAACCGCTTTTATTAATTTTAAATCTGAGTAAATATATATATCAG | 1556 |
| QY | 1561 | TATATCGAAAGCAATATATCTTTGTTAAACAGCGTTGCGTCAATGGAAGTTCAATG | 1620 |
| Db | 1557 | TATATCGAAAGCAATATATCTTTGTTAAACAGCGTTGCGTCAATGGAAGTTCAATG | 1616 |
| QY | 1621 | TGATATCAATAGTTTATATATTAATAAGTAAATTTTAAATTTAATTTTGTATTTTGTTCAGA | 1680 |
| Db | 1617 | TGATATCAATAGTTTATATATTAATAAGTAAATTTTAAATTTAATTTTGTATTTTGTTCAGA | 1676 |
| QY | 1681 | AATTTAAATAATAATTAATTAAGCATGGGAGTTCCGGGACATTAATGAGACACTAGACT | 1740 |
| Db | 1677 | AATTTAAATAATAATTAATTAAGCATGGGAGTTCCGGGACATTAATGAGACACTAGACT | 1736 |
| QY | 1741 | GTTTGAACAAATATATATGTCGATCTTAATGACCTTTCACTCAATATGATTAAT | 1800 |
| Db | 1737 | GTTTGAACAAATATATATGTCGATCTTAATGACCTTTCACTCAATATGATTAAT | 1796 |
| QY | 1801 | GCATTTAGAAATACATCTTTTCAAAATTTCAACAAACACAGCTTTACCTTTCTTCAAG | 1860 |
| Db | 1797 | GCATTTAGAAATACATCTTTTCAAAATTTCAACAAACACAGCTTTACCTTTCTTCAAG | 1856 |

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| QY | 1861 | SATTCGAAATCCCTTTCTTAACTTTTAAATPAAAAAAAAAATCATTTATGTAATATTATC | 1920 |
| Db | 1857 | GATTTGGAAATCCCTTTCTTAACTTTTAAATPAAAAAAAAAATCATTTATGTAATATTATC | 1916 |
| QY | 1921 | AACACCTCAACATTGATGTGACGACATATAATAGGCGCTCTGGTGCTCTACTATCAT | 1980 |
| Db | 1917 | AACACCTCAACATTGATGTGATTTAGCGTACTATAAATAGGCGCTCTGGTGCTCTACTATCAT | 1976 |
| QY | 1961 | CACATCAATCTTAAACCAACAACCTTGAGCTTAATTTTCTACTTATTTCTCAGCAATTAAC | 2040 |
| Db | 1977 | CACATCAATCTTAAACCAACAACCTTGAGCTTAATTTTCTACTTATTTCTCAGCAATTAAC | 2036 |
| QY | 2041 | ATTCGAAATATTC 2052 | |
| Db | 2037 | ATTCGAAATATTC 2048 | |

| | | | | | | |
|------------|--------------------------------------|--------|---------|-----|--------|-----------------|
| RESULT 5 | E40089 | E40089 | 2048 bp | DNA | linear | PAT 31-JAN-2002 |
| LOCUS | E40089 | | | | | |
| DEFINITION | Plant promoter and terminator. | | | | | |
| ACCESSION | E40089 | | | | | |
| VERSION | E40089.1 GI:18627205 | | | | | |
| KEYWORDS | JP 200016577-A/3. | | | | | |
| SOURCE | unidentified | | | | | |
| ORGANISM | unidentified. | | | | | |
| REFERENCE | 1 (bases 1 to 2048) | | | | | |
| AUTHORS | Nishikawa,S. and Oeda,K. | | | | | |
| TITLE | Plant promoter and terminator | | | | | |
| JOURNAL | Patent: JP 200016577-A 3 20-01-2000. | | | | | |

SUMITOMO CHEM CO LTD
OS Daucus carota L.

PN JP 2000166577-A/3
PD 20-JUN-2000
PF 01-OCT-1999 JP 1999281475
PT

PR SATOMI NISHIKAWA, KENJI OEDA
PC C12N5/09, A01H5/00, C12N1/21, C12N5/10// (C12N5/10, C12R1:91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)

| FEATURES | | |
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| CC | Key | Location/Qualifiers |
| PH | promoter | (1)..(2048). |
| FT | Location/Qualifiers | |

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| Best Local Similarity | 99.8% | Pred. No. 5e-307 | | |
| Matches 2047; Conservative | 0 | Mismatches | 1 | Indels 4; Gaps 1 |

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Ddb
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61 CTTCTCTCTTTTGACCTGTTTGATATAAAGAAGTAGAAATATTTTTAAAAAGCTGGAA 120
121 TACTACTTCTCTCTCACAACCTTGGCTTTTTCGAAACCTTATTAACCTTTTACT 180

121 TACTAACTCTCTGCACACTTCGCGTCTTTTCCAAACCTTAATTAATTTTACT 180

181 TCTCATTTTACTCCACTTCTTTTGCTATAGCAAGAAATGCTCTCTTTTACCTTAACCA 240

181 TCATTTCTACTCCATTTCTTCTATATAGCAAGAAATCACTTTTAACTAACCCA 240

241 AACGGCCCTCAATTAAGATCATTCATATAATGTATCTTCAATTTTACGATACCAATACGT 300

Db 241 AACGCCCTCAATTAAGATCATTCATTAATGTATCTTTCATATTTTGGATTAACATACGT 300
QY 301 GAACAGGGTATTTTAAAGTGTCAACAAATCTAATAATTTTACCTGGCGGTGAGA 360
Db 301 GAACAGGGTATTTTAAAGTGTCAACAAATCTAATAATTTTACCTGGCGGTGAGA 360
QY 361 CCGTCTTCCAGATTAATATTTTAAATTTTGTAGCTCCCTTTTAAACAAATTCGATGC 420
Db 361 CCGTCTTCCAGATTAATATTTTAAATTTTGTAGCTCCCTTTTAAACAAATTCGATGC 420
QY 421 AGGACGACTTAGGTGAATACACTGTAGTGAAGCTTTTAAACAAAGAAAGAGTGGTTC 480
Db 421 AGGACGACTTAGGTGAATACACTGTAGTGAAGCTTTTAAACAAAGAAAGAGTGGTTC 480
QY 481 ATGCTCAGCATCAAAATTTGAACAAACCCGACCAACACTCTATCCACGTACTATCTTT 540
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Db 721 TGGTCACTGATTAATAGTATATGTATTAATATAGTAGATCTACATGACATTAAT 780
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Db 1197 AAAAGGAAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATATGATGATTTAG 1256
QY 1261 AAAAGTATGAAAGTATGAGGTGGGTGAGATTTTATATATTAATTAATTTCTATTTG 1320
Db 1257 AAAAGTATGAAAGTATGAGGTGGGTGAGATTTTATATATTAATTAATTTCTATTTG 1316
QY 1321 AGAAAGTTTGAATGTATAGAAATGAGTGGACATCCATAAAGAAAGTATAGAAAT 1380
Db 1317 AGAAAGTTTGAATGTATAGAAATGAGTGGACATCCATAAAGAAAGTATAGAAAT 1376

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QY 1801 GCATTTCAATATACATCTTTTCAAAATTTTCAACAAACACAGCTTTTCACTTTTCAACG 1860
Db 1797 GCATTTCAATATACATCTTTTCAAAATTTTCAACAAACACAGCTTTTCACTTTTCAACG 1856
QY 1861 GATTTGAATCTTTTCTTAACCTTTTAAATTAATAAATGATTTTGTATTTATTC 1920
Db 1857 GATTTGAATCTTTTCTTAACCTTTTAAATTAATAAATGATTTTGTATTTATTC 1916
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Db 1917 AACACCTCAACATGATGTAGTACGTAATTAATGATGCTCTGCTGCTCACTATCAT 1976
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Db 1977 CACATCAATCTTACACCAACCAACCTTGAAGCTTAATTTTCTACTTATTTCTAGCATATAC 2036
QY 2041 ATTCTPAATATC 2052
Db 2037 ATTCTPAATATC 2048

RESULT 6
AR076817 2042 bp DNA linear PAT 30-AUG-2000
LOCUS AR076817
DEFINITION Sequence 2 from patent US 5959176.
ACCESSION AR076817
VERSION AR076817.1 GI:10003563
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2042)
AUTHORS Torikai, S. and Oeda, K.
TITLE Plant promoter and utilization thereof
JOURNAL Patent: US 5959176-A 2 28-SEP-1999; ✓
FEATURES
source location/DnaI1ifiers
1..2042
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Query Match 11.8%; Score 241.2; DB 6; Length 2042;
Best Local Similarity 72.8%; Pred. No. 3,7e-28;
Matches 367; Conservative 0; Mismatches 126; Indels 9; Gaps 4;

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QY 1554 AAATCAGTTATCTGAAAGCAATATATCTTTGTAAACAGCG-----TTGGGTCAAAATG 1609
DB 1543 AAATATTTATCTGATATATATACATCTTTGTAAACAAACGGGCCAAATAGACCATTA 1602
QY 1610 GGAAGTTATCTGATATCAATAGTTTAAATATAAAGTAATTTTAAATTTTAAATTTTAT 1669
DB 1603 CCAAGTTCAAGGTATCTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTT 1660
QY 1670 TTGTTTCAGAAATTTTAAATTAATTTTATGACATGGGAAAGTTTACGGGCATCATTTGAGC 1729
DB 1661 ATAGTTATTTCTTCAATCAATTAATTTTAAATTTTGTACATTAATTTGACCACTTTATGCC 1720
QY 1730 AGCACTAGCTGTTTGAACAAATGATGTCGGGTGATCATCTTAACCTTTCACTCAAC 1789
DB 1721 CAGGTGTATTTGTTTAAACAAAGTTTGTGGGTATTTATTTGACCTTTCACTCAAGC 1780
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QY 1849 TTTCCTTCAACGGAATGGAATCCTTTTCTAACTTTTAAATTTTAAATTTTAAATTTTAA 1908
DB 1841 TTTCCTTTTAAACAGATTAAGATGTTTCTTAACTTTTAAATTTTAAATTTTAAATTTTAA 1908
QY 1909 GTAATATTTATCAACACCTTCAACATTTGATGTTAGGTTACTATTAATAGTGTCTTTGGTG 1968
DB 1899 ATTAATTTTATCAACACCTTCAACATTTGATGTTAGGTTACTATTAATAGTGTCTTTGGTG 1958
QY 1969 CTCCTATCATCATCATCATCATCTTACACCAAACTTGAAGCTTAATTTTCTTACTTAT 2028
DB 1959 CTCCTATCATCATCATCATCATCTTACACCAAACTTGAAGCTTAATTTTCTTACTTAT 2018
QY 2029 CTCAGCAATTAACATTTCTAAATATC 2052
DB 2019 TTAGCAAAACATTTCTAAAGTC 2042

RESULT 7
E15125 LOCUS E15125 2042 bp DNA linear PAT 28-JUL-1999
DEFINITION Promoter.
ACCESSION E15125
VERSION E15125.1 GI:5709808
KEYWORDS JP 1998052273-A/2.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2042)
AUTHORS Torikai,T. and Ohta,K.
TITLES VEGETABLE PROMOTER AND ITS USE
JOURNAL Patent: JP 1998052273-A 2 24-FEB-1998;
SOMITOMO CHEM CO LTD
COMMENT OS Daucus carota L. (carrot)
PN JP 1998052273-A/2
PD 24-FEB-1998
PF 12-AUG-1996 JP 1996212680
PI TORIKAI,TOSHIMI, OHTA,KENJI
PC C12N15/09,A01H5/00,C07H21/04,C07K14/415,C12N1/21,C12N5/10,CC
Strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..2042
FT promoter 1<..<2042.
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ORIGIN
Query Match 11.8%; Score 241.2; DB 6; Length 2042;
Best Local Similarity 72.8%; Pred. No. 3,7e-28;
Matches 367; Conservative 0; Mismatches 128; Indels 9; Gaps 4;

QY 1554 AAATCAGTTATCTGAAAGCAATATATCTTTGTAAACAGCG-----TTGGGTCAAAATG 1609
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QY 1610 GGAAGTTATCTGATATCAATAGTTTAAATATAAAGTAATTTTAAATTTTAAATTTTAT 1669
DB 1603 CCAAGTTCAAGGTATCTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTT 1660
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QY 2029 CTCAGCAATTAACATTTCTAAATATC 2052
DB 2019 TTAGCAAAACATTTCTAAAGTC 2042

RESULT 8
AR076816 LOCUS AR076816 247 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 1 from patent US 5959176.
ACCESSION AR076816
VERSION AR076816.1 GI:10003562
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 247)
AUTHORS Torikai,S. and Oeda,K.
TITLES Plant promoter and utilization thereof
JOURNAL Patent: US 5959176-A 1 28-SEP-1999;
FEATURES
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Location/Qualifiers
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Query Match 9.6%; Score 196.6; DB 6; Length 247;
Best Local Similarity 89.6%; Pred. No. 4.9e-21;
Matches 223; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

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DB 1 TTCTAGAAATATCTTTTGAATTTTCAACAAACAGCACTTAACTTTCTTTTAAAGAT 60
QY 1864 TGAATCCTTTTCAACCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1923

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Db 61 TAGAATCGTTCTTAACTTTTAAAT--AAAAATACATTACTATAATTTATCAAC 118
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Db 119 ACCGACATGATGTAGCGTACTATAATAGTGTCTGTGCTCTACTATCATCAGC 178
Qy 1984 ATCAATCTTACACCAAACTTGAAGCTTAATTTTCTACTTAATTTCTCAGCAATACAT 2043
Db 179 ATCAATCTTCCAGCAAACTTGAAGCTTAATTTTCTACTTAATTTTGAACAAAACATT 238
Qy 2044 CTAATATTC 2052
Db 239 CTAAGGTC 247
RESULT 9
E5124 247 bp DNA linear PAT 28-JUL-1999
LOCUS Promoter.
DEFINITION E5124
ACCESSION E5124.1 GI:5709807
VERSION JP 1998052273-A/1.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 247)
AUTHORS Torikata, T. and Ohta, K.
TITLE VEGETABLE PROMOTER AND ITS USE
JOURNAL Patent: JP 1998052273-A 1 24-FEB-1998;
SUMITOMO CHEM CO LTD
OS Daucus carota L. (carrot)
PN JP 1998052273-A/1
PD 24-FEB-1998
PF 12-AUG-1998 JP 1996212680
PI TORIKATA TOSHIMI, OHTA KENJI
PC C12N15/09,A01H5/00,C07H21/04,C07K14/415,C12N1/21,C12N5/10; CC
strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
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ORIGIN
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Best Local Similarity 89.6%; Pred. No. 4.9e-21;
Matches 223; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
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Db 1 TTCTAGAATATATCTTTGAAATTTCAACAAACAGCACTTAATCTTTTAAACAGAT 60
Qy 1864 TGGATTCCTTTCTTAACTTTTAAATAAAAATGCAATTTCTATATTTATTAACAAC 1923
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Qy 2044 CTAATATTC 2052
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RESULT 10
AR146852 246 bp DNA linear PAT 08-AUG-2001
LOCUS AR146852
DEFINITION Sequence 2 from patent US 6218598.
ACCESSION AR146852
VERSION AR146852.1 GI:15110041
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 246)
AUTHORS Ishige, F., Nishikawa, S. and Oeda, K.
TITLE Plant promoter
JOURNAL Patent: US 6218598-A 2 17-APR-2001;
LOCATION/Qualifiers
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Best Local Similarity 89.5%; Pred. No. 7e-21;
Matches 222; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
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Qy 1865 GGAATCTTTTCTTAACTTTTAAATAAAAATGCAATTTGTAATTTATTAACAAC 1924
Db 61 AGAATCGTTTCTTAACTTTTAAAT--AAAAATACATTACTATAATTTATCAACA 118
Qy 1925 CCTCAATGATGTAGCGTACTATAATAGTGTCTGTGCTCTACTATCATCACA 1984
Db 119 CCTCAATGATGTAGCGTACTATAATAGTGTCTGTGCTCTACTATCATCACA 178
Qy 1985 TCAATCTTACACCAAACTTGAAGCTTAATTTTCTACTTAATTTCTCAGCAATACATT 2044
Db 179 TCAATCTTCCAGCAAACTTGAAGCTTAATTTTCTACTTAATTTTGAACAAAACATT 238
Qy 2045 TAAATATC 2052
Db 239 TAAAGGTC 246
RESULT 11
E55065 246 bp DNA linear PAT 31-JAN-2002
LOCUS E55065
DEFINITION Plant promoter.
ACCESSION E55065
VERSION E55065.1 GI:18625251
KEYWORDS JP 2000083679-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 246)
AUTHORS Ishige, F., Nishikawa, S. and Oeda, K.
TITLE Plant promoter
JOURNAL Patent: JP 2000083679-A 2 28-MAR-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
PN JP 2000083679-A/2
PD 28-MAR-2000
PF 12-JUL-1999 JP 1999197240
PI IKUHARU ISHIGE, SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,C12N5/10/(C12N15/09,C12R1:91), PC
(C12N5/10,C12R1:91), C12N15/00,C12N5/00,(C12N15/00,C12R1:91), PC

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Best Local Similarity 89.5%; Pred. No. 76-21; Mismatches 24; Indels 2; Gaps 1;
Matches 222; Conservative 0;
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DB 61 AAGATCGTTCTTAACTTTTAAAT--AAAAATACATTACTATATATTATCAACA 118
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QY 2045 TAAATATC 2052
DB 239 TAAAGGTC 246
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LOCUS DCA18706 8005 bp DNA linear PLN 10-FEB-1999
DEFINITION Daucus carota Inv*Dc5 gene.
ACCESSION Y18706
VERSION Y18706.1 GI:4454114
KEYWORDS beta-fructofuranosidase; Inv*Dc5 gene; invertase; isoform.
SOURCE Daucus carota (carrot)
ORGANISM Daucus carota
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Asteridae; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
    Daucinae; Daucus.
1
REFERENCE
    1 Sturm,A.
        Molecular characterisation and functional analysis of
        sucrose-cleaving enzymes in carrot (Daucus carota L.)
        J. Exp. Bot. 47, 1187-1192 (1996)
2 (bases 1 to 8005)
    1 Sturm,A.
        Direct Submission
        Submitted (27-JAN-1999) A. Sturm, Friedrich Miescher-Institut,
        Maulbeerstr. 66, CH-4058 Basel, SWITZERLAND
COMMENT
    Related sequence X67163.
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    77 CCTGTTTGTATTAAGAGTAGAAATATTTTAAAAAGCTCGAATACTACTCTCTCTC 136
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Db 1225 CCGGTTGTGTAATAAGCAGAGCAATTTTAAAAAGTGAAGATCTAGCTTCTCTC 1166
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Db 1165 AAGGCTTCGCTTCTTTCCAAACACTTTATTAATTTTACTTTCTCATTTCTCTCA 1106
Qy 197 CTTCTTGTATAGCAAGAAATCACTTCTTTTAAGCTAACCCAAAGGCTCAATATAA 256
Db 1105 CTTTCTATTTAAGTAAGAAATCACTTCTTTTAAGCTAACCCAAAGGCTCAATAGCT 1046
Qy 257 GATCAT 262
Db 1045 GACCCCT 1040

RESULT 13
LOCUS BD188672 2831 bp DNA linear PAT 17-JUL-2003
DEFINITION Promotor and use thereof.
ACCESSION BD188672
VERSION BD188672.1 GI:32998411
KEYWORDS JP 2003000252-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2831)
AUTHORS Nishikawa, S. and Oeda, K.
TITLE Promotor and use thereof
JOURNAL Patent: JP 2003000252-A 1 07-JAN-2003;
SUMITOMO CHEMICAL CO LTD
COMMENT OS Daucus carota L. (carrot)
PN JP 2003000252-A/1
PD 07-JAN-2003
PF 31-MAY-2001 JP 2001164069
PI SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N5/00
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Best Local Similarity 82.5%; Pred. No. 6.4e-16;
Matches 198; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

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Qy 82 TTGTATAAAGAGTAGAATATTTTAAAAAGTGGAAATCAATCTTCTCTCAAC 141
Db 1775 TTGTATAAAGAGTAGAATATTTTAAAAAGTGGAAATCAATCTTCTCTCAAC 1834
Qy 142 TTCGCTTCTTTCCAAACCTTTATTAATTTTACTTCTCATTTCTTCACTTCTCACTTCT 201
Db 1835 TTCGCTTCTTTCCAAACCTTTATTAATTTTACTTCTCATTTCTTCACTTCTCACTTCT 1894
Qy 202 TTGCTATAAGCAAGAAATCACTTCTTTAAGCTAACCCAAAGGCTCAATATAAGATCA 261
Db 1895 TTACTATAAGCAAGAAATCACTTCTTTAAGCTAACCCAAAGGCTCAATATAAGATCA 1954

RESULT 14
LOCUS BD188674 2865 bp DNA linear PAT 17-JUL-2003
DEFINITION Promotor and use thereof.

ACCESSION BD188674
VERSION BD188674.1 GI:32998413
KEYWORDS JP 2003000252-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2865)
AUTHORS Nishikawa, S. and Oeda, K.
TITLE Promotor and use thereof
JOURNAL Patent: JP 2003000252-A 3 07-JAN-2003;
SUMITOMO CHEMICAL CO LTD
COMMENT OS Daucus carota L. (carrot)
PN JP 2003000252-A/3
PD 07-JAN-2003
PF 31-MAY-2001 JP 2001164069
PI SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/10, C12N5/00
CC Promotor and use thereof
FH Key Location/Qualifiers
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ORIGIN
Query Match 7.9%; Score 162.4; DB 6; Length 2865;
Best Local Similarity 82.5%; Pred. No. 6.4e-16;
Matches 198; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 22 AGGCGCTGTTGGTGAAGAGCAGAGCTGCTTCTGACTTCTTCTTTGACCTGT 81
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Qy 82 TTGTATAAAGAGTAGAATATTTTAAAAAGTGGAAATCAATCTTCTCTCAAC 141
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Qy 142 TTCGCTTCTTTCCAAACCTTTATTAATTTTACTTCTCATTTCTTCACTTCT 201
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Qy 202 TTGCTATAAGCAAGAAATCACTTCTTTAAGCTAACCCAAAGGCTCAATATAAGATCA 261
Db 1895 TTACTATAAGCAAGAAATCACTTCTTTAAGCTAACCCAAAGGCTCAATATAAGATCA 1954

RESULT 15
LOCUS DARGCHS2 4886 bp DNA linear PLN 14-APR-2000
DEFINITION Carrot gchs2 gene for chalcone synthase.
ACCESSION D16255
VERSION D16255.1 GI:441168
KEYWORDS chalcone synthase.
SOURCE Daucus carota (carrot)
ORGANISM Daucus carota
REFERENCE 1 (bases 1 to 4886)
AUTHORS Ozeki, Y., Davies, E. and Takeda, J.
TITLE Structure and expression of chalcone synthase gene in carrot
JOURNAL suspension cultured cells regulated by 2,4-D
Plant Cell Physiol. 34, 1029-1037 (1993)
REFERENCE 2 (bases 1 to 4886)
AUTHORS Ozeki, Y.
TITLE Direct Submision
JOURNAL Submitted (14-MAY-1993) Yoshihiro Ozeki, College of Arts and Sciences, The University of Tokyo, Department of Biology, Komaba, Meguro-ku, Tokyo 153, Japan (Tel:03-3467-1171(ex.253),

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-806-197-1

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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12: geneseqn20048s:*
13: geneseqn20048s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2048.8 | 99.8 | 2052 | 3 | AAA37961 Carrot pr |
| 3 | 2034.8 | 99.2 | 2056 | 3 | AAA37964 Carrot pr |
| 4 | 2030.8 | 99.0 | 2048 | 3 | AAA37962 Carrot pr |
| 5 | 2030.8 | 99.0 | 2048 | 3 | AAA37963 Carrot pr |
| 6 | 239.6 | 11.7 | 2042 | 2 | AAV15144 New Promo |
| 7 | 196.6 | 9.6 | 247 | 2 | AAV15143 New Promo |
| 8 | 195.6 | 9.5 | 246 | 2 | AAZ49611 Carrot CR |
| 9 | 194.4 | 9.5 | 196 | 12 | ADP07499 Carrot DN |
| 10 | 162.4 | 7.9 | 2831 | 10 | ADCS6759 Carrot DN |
| 11 | 162.4 | 7.9 | 2865 | 10 | ADCS6761 Carrot DN |
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| 13 | 119 | 5.8 | 140 | 3 | AAZ49615 Oligonuc |
| 14 | 99.4 | 4.8 | 8056 | 8 | ABZ10246 Haematopo |
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| 19 | 87.2 | 4.2 | 110000 | 13 | ABD32968 6 of |
| 20 | 83 | 4.0 | 158001 | 12 | ADL17884 Human pho |

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| C | 27 | 69.8 | 3.4 | 6352 | 6 | ABK31340 Signal tr |
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| C | 31 | 69.6 | 3.4 | 11222 | 10 | ADB54190 Pretreat |
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ALIGNMENTS

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ID AAA37959 standard; DNA; 2052 BP.
XX AAA37959;
AC
XX
DT 18-AUG-2000 (first entry)
DE Carrot promoter sequence #1.
XX
XX Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds.
XX Daucus carota.
OS
XX
PN WO200020613-A1.
XX
PD 13-APR-2000.
XX
PF 28-SEP-1999; 99WO-JP005303.
XX
PR 02-OCT-1998; 98JP-00281124.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Nishikawa S, Oeda K;
XX WPI, 2000-303791/26.
XX
PT New Plant promoters and terminators from *Daucus carota* L., useful in
XX plant breeding, for e.g. controlling fertilities of plants.
XX
PS Claim 1, Page 69-70; 81pp; English.
XX
XX This sequence represents a carrot promoter. The invention relates to
XX plant promoters and terminators from *Daucus carota* L., which are capable
XX of expressing a gene of interest in plants. The invention also includes a
XX chimeric gene characterized in that it comprises the promoter and a
XX desired gene linked to each other in the form capable of functioning. A
XX method of producing a transformant comprises introducing the promoter,
XX the chimeric gene or a vector comprising the promoter and a desired gene
XX or terminator sequence into a host cell. The plant promoters and
XX terminators are useful in plant breeding, for e.g. fertilities of plants
XX may be controlled by expressing, in the host cells, a sense or antisense

CC gene of a male sterility related gene such as S-locus-specific RNase gene
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Query Match 100.0%; Score 2052; DB 3; Length 2052;
 Best Local Similarity 100.0%; Pred. No. 0;
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DB 1681 AATTTAAATTAATATATATATATATATATATATATATATATATATATATATATAT 1740
QY 1741 GTTTGAACAGTATATGTCGGGTATCATATATGACCTTTCAACTCAACTAGTAAATAT 1800
DB 1741 GTTTGAACAGTATATGTCGGGTATCATATATGACCTTTCAACTCAACTAGTAAATAT 1800
QY 1801 GCATTTCTGAATATACATCTTTCAATTTCAACAAACAGCTTAAATTTTCTTCAAG 1860
DB 1801 GCATTTCTGAATATACATCTTTCAATTTCAACAAACAGCTTAAATTTTCTTCAAG 1860
QY 1861 GATTTGAAATCTTTTCTTAACTTTTAAATTAATAAATATGCAATTTTGAATATATAT 1920
DB 1861 GATTTGAAATCTTTTCTTAACTTTTAAATTAATAAATATGCAATTTTGAATATATAT 1920
QY 1921 AACACCTCAACATGATGATAGGATCATATATATATATATATATATATATATATAT 1980
DB 1921 AACACCTCAACATGATGATAGGATCATATATATATATATATATATATATATATAT 1980
QY 1981 CAGATCATCTTACACCAACCTTGAAGCTTAATTTTCTACTTAATTTCTCAGCAATATAC 2040
DB 1981 CAGATCATCTTACACCAACCTTGAAGCTTAATTTTCTACTTAATTTCTCAGCAATATAC 2040
QY 2041 ATTCTAATATATC 2052

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DB 2041 ATTCTAAATATC 2052

RESULT 2
ID AAA37961 standard; DNA; 2052 BP.
AC AAA37961;
XX
XX 18-AUG-2000 (first entry)
XX
XX Carrot promoter sequence #2.
DE Carrot promoter; terminator; transgenic plant; breeding; fertility; ds.
XX
XX Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds.
XX Daucus carota.
XX
XX WO200020613-A1.
XX
XX 13-APR-2000.
XX
XX 28-SEP-1999; 99WO-JP005303.
XX
XX 02-OCT-1998; 98JP-00281124.
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Nishikawa S, Oeda K;
XX
XX WPI; 2000-303791/26.
XX
XX New Plant promoters and terminators from Daucus carota L., useful in
XX plant breeding, for e.g. controlling fertilities of plants.
XX
XX Claim 1; Page 78-79; 81pp; English.

This sequence represents a carrot promoter. The invention relates to
CC plant promoters and terminators from Daucus carota L. which are capable
CC of expressing a gene of interest in plants. The invention also includes a
CC chimeric gene characterized in that it comprises the promoter and a
CC desired gene linked to each other in the form capable of functioning. A
CC method of producing a transformant comprises introducing the promoter,
CC the chimeric gene or a vector comprising the promoter and a desired gene
CC or terminator sequence into a host cell. The plant promoters and
CC terminators are useful in plant breeding, for e.g. fertilities of plants
CC may be controlled by expressing, in the host cells, a sense or antisense
CC gene of a male sterility related gene such as S-locus-specific RNase gene
CC
XX
XX Sequence 2052 BP; 736 A; 318 C; 317 G; 681 T; 0 U; 0 Other;

Query Match 99.8%; Score 2048.8; DB 3; Length 2052;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2050; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATGTCGTCCTACAGACATAGAGCGCTGTTGGTTGAGAGAAAGCAGAGCTGCTTGA 60
DB 1 CATGTCGTCCTACAGACATAGAGCGCTGTTGGTTGAGAGAAAGCAGAGCTGCTTGA 60
QY 61 CTTCTCTCTCTTTGACCTGTTGTAATAAGAAAGTAAGAAATATTTTAAAAAGCTGCGAA 120
DB 61 CTTCTCTCTCTTTGACCTGTTGTAATAAGAAAGTAAGAAATATTTTAAAAAGCTGCGAA 120
QY 121 TACTAATCTCTCTCTACAACTTCGCTCTTTTCCAAACATTATTTAACTTTTACT 180
DB 121 TACTAATCTCTCTCTACAACTTCGCTCTTTTCCAAACATTATTTAACTTTTACT 180
QY 181 TCTCATTTTCTACCTCTCTTGTCTATAGCAAGAAATCACTTCTTTAAGCTAACCA 240
DB 181 TCTCATTTTCTACCTCTCTTGTCTATAGCAAGAAATCACTTCTTTAAGCTAACCA 240
QY 241 AACGCGCTCAATPAAAAAGATCATTCATPAAATGTATCTTTCAATTTTNGATPAAATAGCT 300
DB 241 AACGCGCTCAATPAAAAAGATCATTCATPAAATGTATCTTTCAATTTTNGATPAAATAGCT 300

QY 301 GAAACAGGTTATTTTAAAGTGTCAACAAATTCATATATTTTACGTGGCCGGTGAACA 360
DB 301 GAAACAGGTTATTTTAAAGTGTCAACAAATTCATATATTTTACGTGGCCGGTGAACA 360
QY 361 CCGTCTTCCAGATTAATATTTTAAATTTTGAGTACCTCCCTTTTAAACAAATTCGATGC 420
DB 361 CCGTCTTCCAGATTAATATTTTAAATTTTGAGTACCTCCCTTTTAAACAAATTCGATGC 420
QY 421 AGAGACATTTAGTGAATACATTTGTACTGTGAGCTTTTAAACAAAGAAAGATGTTTC 480
DB 421 AGAGACATTTAGTGAATACATTTGTACTGTGAGCTTTTAAACAAAGAAAGATGTTTC 480
QY 481 ATGCTCAGCCATCAAAATTTGACAAACCCGACACAACTCTATCCAGCTATATCTTT 540
DB 481 ATGCTCAGCCATCAAAATTTGACAAACCCGACACAACTCTATCCAGCTATATCTTT 540
QY 541 TGGCCGAATGCTTCTCAAAATGTTTTTATATGTAAATPAAATGCGCATCCAAAGATPAGT 600
DB 541 TGGCCGAATGCTTCTCAAAATGTTTTTATATGTAAATPAAATGCGCATCCAAAGATPAGT 600
QY 601 AAAATTCCTGGTTTAAACAGTTTGTATATATATGTTTACATTACAAAGATATTCGT 660
DB 601 AAAATTCCTGGTTTAAACAGTTTGTATATATATGTTTACATTACAAAGATATTCGT 660
QY 661 AATACTTTTGAAGCAAGACCTTAGTCAAAAATGACGCTGTGTAACAGCTTAGCT 720
DB 661 AATACTTTTGAAGCAAGACCTTAGTCAAAAATGACGCTGTGTAACAGCTTAGCT 720
QY 721 TGGTCACTGATTAATGATTAATGTTAGTATATATATAGATCTTCAATGACATTTAA 780
DB 721 TGGTCACTGATTAATGATTAATGTTAGTATATATATAGATCTTCAATGACATTTAA 780
QY 781 ATTAGAGCTTATTAATTAAGTACTAATTAATTAAGAGAGGTAGTAAACGAAAGCGTA 840
DB 781 ATTAGAGCTTATTAATTAAGTACTAATTAATTAAGAGAGGTAGTAAACGAAAGCGTA 840
QY 841 AAAACAGAGCTTGTGCTGTGTGTTAGTTGTTGAGCTCACTTTCTTAAAAAGTATG 900
DB 841 AAAACAGAGCTTGTGCTGTGTGTTAGTTGTTGAGCTCACTTTCTTAAAAAGTATG 900
QY 901 TTAACGATCTTAAGACATAGAAATTTAGTACAGTTTAACTTTTACAGATTTTAA 960
DB 901 TTAACGATCTTAAGACATAGAAATTTAGTACAGTTTAACTTTTACAGATTTTAA 960
QY 961 TTAACGAAATCATTTTAAACATGCTCTGCGCTGATTTAATAGGATCACTTAC 1020
DB 961 TTAACGAAATCATTTTAAACATGCTCTGCGCTGATTTAATAGGATCACTTAC 1020
QY 1021 TGATCATTCATTAACCTGTTTAAACAAATTCATAGATPAAATATCTTACATGAA 1080
DB 1021 TGATCATTCATTAACCTGTTTAAACAAATTCATAGATPAAATATCTTACATGAA 1080
QY 1081 AAGAAGCAATGCTCTTTGAAAAAACAATAGTACTCCCTCCCTCTGAAATGT 1140
DB 1081 AAGAAGCAATGCTCTTTGAAAAAACAATAGTACTCCCTCCCTCTGAAATGT 1140
QY 1141 ATACATATGATTTGACACGAGACTTACAGAAAAATGTATTAAGTATGTAGGTAAG 1200
DB 1141 ATACATATGATTTGACACGAGACTTACAGAAAAATGTATTAAGTATGTAGGTAAG 1200
QY 1201 AAAAGAAAAGAAAGGTGTAAGTAGGCGGACCCACCAATATPAAATGATGATTTAG 1260
DB 1201 AAAAGAAAAGAAAGGTGTAAGTAGGCGGACCCACCAATATPAAATGATGATTTAG 1260
QY 1261 AAAAGATTTGAAGTAGTGCGGTGGGATTTTATATTAATAAATTTTACTATTTTG 1320
DB 1261 AAAAGATTTGAAGTAGTGCGGTGGGATTTTATATTAATAAATTTTACTATTTTG 1320
QY 1321 AGAAAGTTTGAATGTATAGAAATGAGTGGACATCCATAAAGAAAGTATAGAAAT 1380
DB 1321 AGAAAGTTTGAATGTATAGAAATGAGTGGACATCCATAAAGAAAGTATAGAAAT 1380

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| XX | RESULT 3 |
| XX | AAA37964 |
| XX | AAA37964 standard; DNA; 2056 BP. |
| XX | AAA37964; |
| XX | 18-AUG-2000 (first entry) |
| XX | Plasmid #3 DNA sequence used in mutation of promoter sequence. |
| XX | Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds. |
| XX | Daucus carota. |
| XX | WO200020613-A1. |
| XX | 13-APR-2000. |
| XX | 28-SEP-1999; 99WO-JP005303. |
| XX | 02-OCT-1998; 98JP-00281124. |
| XX | (SUMO) SUMITOMO CHEM CO LTD. |
| XX | |

| | | | | |
|----------------------------|--------|---------------|-------|--------------|
| Query-Match | 99.2% | Score 2034.8; | DB 3; | Length 2056; |
| Best Local Similarity | 99.7%; | Pred. No. 0; | | |
| Matches 2050; Conservative | 0; | Mismatches | 3 | 7-2-1 |

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 52 |
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|--|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|

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Db      ||| 661 ||| 720
Qy      ||| 721 ||| 780
Db      ||| 721 ||| 780
Qy      ||| 781 ||| 840
Db      ||| 781 ||| 840
Qy      ||| 841 ||| 900
Db      ||| 841 ||| 900
Qy      ||| 901 ||| 960
Db      ||| 901 ||| 960
Qy      ||| 961 ||| 1020
Db      ||| 961 ||| 1020
Qy      ||| 1021 ||| 1080
Db      ||| 1021 ||| 1080
Qy      ||| 1081 ||| 1140
Db      ||| 1081 ||| 1140
Qy      ||| 1141 ||| 1200
Db      ||| 1141 ||| 1200
Qy      ||| 1201 ||| 1260
Db      ||| 1201 ||| 1260
Qy      ||| 1261 ||| 1320
Db      ||| 1261 ||| 1320
Qy      ||| 1321 ||| 1380
Db      ||| 1321 ||| 1380
Qy      ||| 1381 ||| 1440
Db      ||| 1381 ||| 1440
Qy      ||| 1441 ||| 1500
Db      ||| 1441 ||| 1500
Qy      ||| 1501 ||| 1560
Db      ||| 1501 ||| 1560
Qy      ||| 1561 ||| 1620
Db      ||| 1561 ||| 1620
Qy      ||| 1621 ||| 1680
Db      ||| 1621 ||| 1680
Qy      ||| 1681 ||| 1740
Db      ||| 1681 ||| 1740
Qy      ||| 1741 ||| 1800
Db      ||| 1741 ||| 1800

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Db      1741 GTTGAACAATGATGTCGGGTGATCATCTATGACCTTTCACCTCAACTAGTAAT 1800
Qy      1801 GCATT-----CTAGAAATACCTTTTCAATTTCAACAAACAGAGCTTTACTTTCTTC 1856
Db      1801 GCATTCTAGCTGAAATACCTTTTCAATTTCAACAAACAGAGCTTTACTTTCTTC 1860
Qy      1857 AACGATTTGGAATCCCTTTCTAACTTTTAAATTAATAATGATTAATTTGTAAT 1916
Db      1861 AAGGATTTGGAATCCCTTTCTAACTTTTAAATTAATAATGATTAATTTGTAAT 1920
Qy      1917 TATCAACACCTCAACATTGATGTAGCGGATTAATAATGAGTCTTGTGCTCTACTA 1976
Db      1921 TATCAACACCTCAACATTGATGTAGCGGATTAATAATGAGTCTTGTGCTCTACTA 1980
Qy      1977 TCATCATCATATCTTTACACCAACCTTGAGCTTAATTTTCTACTAATCTCAGCA 2036
Db      1981 TCATCATCATATCTTTACACCAACCTTGAGCTTAATTTTCTACTAATCTCAGCA 2040
Qy      2037 TAACATTTCAATATATC 2052
Db      2041 TCACATTTCAATATATC 2056

RESULT 4
AAA37962
ID AAA37962 standard; DNA; 2048 BP.
XX
AC AAA37962;
XX
DT 18-AUG-2000 (first entry)
XX
DE Plasmid #1 DNA sequence used in mutation of promoter sequence.
XX
KW Carrot; promoter; terminator; transgenic plant; breeding; fertility; da.
XX
OS Daucus carota.
XX
PN MO200020613-A1.
XX
PD 13-APR-2000.
XX
PF 28-SEP-1999; 99WO-JP005303.
XX
PR 02-OCT-1998; 96UP-0028124.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI Nishikawa S, Oeda K;
XX
DR WPI; 2000-303791/26.
XX
PT New Plant promoters and terminators from Daucus carota L., useful in
XX plant breeding, for e.g. controlling fertilities of plants.
XX
PS Example 8; Page 71-73; 81pp; English.
XX
CC This sequence represents a plasmid sequence used in a method for
CC introducing a mutation into a carrot promoter. The invention relates to
CC plant promoters and terminators from Daucus carota L. which are capable
CC of expressing a gene of interest in plants. The invention also includes a
CC chimeric gene characterized in that it comprises the promoter and a
CC desired gene linked to each other in the form capable of functioning. A
CC method of producing a transformant comprises introducing the promoter,
CC the chimeric gene or a vector comprising the promoter and a desired gene
CC or terminator sequence into a host cell. The plant promoters and
CC terminators are useful in plant breeding, for e.g. fertilities of plants
CC may be controlled by expressing, in the host cells, a sense or antisense
CC gene of a male sterility related gene such as S-locus-specific RNase gene
XX
SQ Sequence 2048 BP; 735 A; 317 C; 316 G; 680 T; 0 U; 0 Other;

Query Match 99.0%; Score 2030.8; DB 3; Length 2048;
Best Local Similarity 99.7%; Pred. No. 0;

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Matches 2046; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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QY 1 CATGTGCGCCCTACAGCAATAGGCGCTGTTGGTTGAGAGAGAGAGAGCTGCTTGA 60
Db 1 CATGTGCGCCCTACAGCAATAGGCGCTGTTGGTTGAGAGAGAGAGAGCTGCTTGA 60
QY 61 CTTCTCTCTCTTTGACCTGTTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 CTTCTCTCTCTTTGACCTGTTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 TACTAGCTCTCTCAACACTTCGCTCTTTTCCAAACACTTATTAATCTTTTACT 180
Db 121 TACTAGCTCTCTCAACACTTCGCTCTTTTCCAAACACTTATTAATCTTTTACT 180
QY 181 TCTCATTTCTCACTCTCTTCTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 TCTCATTTCTCACTCTCTTCTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 AAGGCGCTCAATTAAGATCATTAATGTAATTTTCAATTTAGATTAACAATAGT 300
Db 241 AAGGCGCTCAATTAAGATCATTAATGTAATTTTCAATTTAGATTAACAATAGT 300
QY 301 GAACAGGCTTAATTTTAAAGTCAACAAATCTTAATTTTAACTGCGCGGTGAACA 360
Db 301 GAACAGGCTTAATTTTAAAGTCAACAAATCTTAATTTTAACTGCGCGGTGAACA 360
QY 361 CCGTCTTCCAAATTAATTTTAAATTTTGTAGCTCCCTTTTAAACCAATTTGCAATG 420
Db 361 CCGTCTTCCAAATTAATTTTAAATTTTGTAGCTCCCTTTTAAACCAATTTGCAATG 420
QY 421 AGGAGACTTAGGTGAATACATATGTAAGTGAATCTTTTAAACCAAGAGAGAGTTC 480
Db 421 AGGAGACTTAGGTGAATACATATGTAAGTGAATCTTTTAAACCAAGAGAGAGTTC 480
QY 481 ATGCTCAGCAATCAAAATTTGACAAACCCGACACAACTCTATCAAGTACTATTTT 540
Db 481 ATGCTCAGCAATCAAAATTTGACAAACCCGACACAACTCTATCAAGTACTATTTT 540
QY 541 TGGCGGAATGCTTCAAAATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 600
Db 541 TGGCGGAATGCTTCAAAATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 600
QY 601 AAAATTCCTTTTAAACAGTTTGTAAATTAATTAATTTTAACTTACAAAGAGATTTGT 660
Db 601 AAAATTCCTTTTAAACAGTTTGTAAATTAATTAATTTTAACTTACAAAGAGATTTGT 660
QY 661 AATTCCTTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 AATTCCTTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 TGGTCACTGATTAATTAATTTTGTATTAATTAATTAATTAATTAATTAATTAAT 780
Db 721 TGGTCACTGATTAATTAATTTTGTATTAATTAATTAATTAATTAATTAATTAAT 780
QY 781 ATTGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
Db 781 ATTGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 AAAACAGAGAGCTTGGCTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
Db 841 AAAACAGAGAGCTTGGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 900
QY 901 TAAATCTGATTAAGACATAGAAATTAAGTAAAGTTAAACCTTTTAAACAGAGATTA 960
Db 901 TAAATCTGATTAAGACATAGAAATTAAGTAAAGTTAAACCTTTTAAACAGAGATTA 960
QY 961 TTAACAGAGAAATCAATTTTAAATCAATGCTGCGCTGTCATTAATTAAGAGATCACTTAC 1020
Db 961 TTAACAGAGAAATCAATTTTAAATCAATGCTGCGCTGTCATTAATTAAGAGATCACTTAC 1020
QY 1021 TGAATCAATCAATTAATCAATTTTAAATCAATGCTGCGCTGTCATTAATTAAGAGATCACTTAC 1080
Db 1021 TGAATCAATCAATTAATCAATTTTAAATCAATGCTGCGCTGTCATTAATTAAGAGATCACTTAC 1080
QY 1017 TGAATCAATCAATTAATCAATTTTAAATCAATGCTGCGCTGTCATTAATTAAGAGATCACTTAC 1076

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QY 1081 AAGAGGACAAATGCTCTTTGAAAAAACAATAGTATCCCTCCGCTCCCTGAAATGT 1140
Db 1077 AAGAGGACAAATGCTCTTTGAAAAAACAATAGTATCCCTCCGCTCCCTGAAATGT 1136
QY 1141 ATACATATGATTTGACACCGAGACTAAGAAAAATGATTAAGTAAATGATGATTAAG 1200
Db 1137 ATACATATGATTTGACACCGAGACTAAGAAAAATGATTAAGTAAATGATGATTAAG 1196
QY 1201 AAGAGGAAAGAAAGTGAGGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1260
Db 1197 AAGAGGAAAGAAAGTGAGGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1256
QY 1261 AAAAGTATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
Db 1257 AAAAGTATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1316
QY 1321 AGAAAGTTTGAATATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1380
Db 1317 AGAAAGTTTGAATATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1376
QY 1381 TAAATGAGACAGAGGAGTAAATACCTTATGATTAATTAATTAATTAATTAATTAAT 1440
Db 1377 TAAATGAGACAGAGGAGTAAATACCTTATGATTAATTAATTAATTAATTAATTAAT 1436
QY 1441 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Db 1437 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1496
QY 1501 CTGATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 1497 CTGATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1556
QY 1561 TTAATGAAAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
Db 1557 TTAATGAAAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1616
QY 1621 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
Db 1617 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1676
QY 1681 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Db 1677 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1736
QY 1741 GTTGAACATGATATGCTGCTGATACATTAATTAATTAATTAATTAATTAATTAAT 1800
Db 1737 GTTGAACATGATATGCTGCTGATACATTAATTAATTAATTAATTAATTAATTAAT 1796
QY 1801 GCATTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1797 GCATTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1856
QY 1861 GATTTGAATTCCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
Db 1857 GATTTGAATTCCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1916
QY 1921 AACACTCAACATGATTAAGTAAAGTAAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1917 AACACTCAACATGATTAAGTAAAGTAAATTAATTAATTAATTAATTAATTAATTAAT 1976
QY 1981 CAGATCAATCTTACACCAACAACTTGAATTAATTTTCTAATTTCTGAGAAATTAAC 2040
Db 1977 CAGATCAATCTTACACCAACAACTTGAATTAATTTTCTAATTTCTGAGAAATTAAC 2036
QY 2041 ATTCTAATTAATTC 2052
Db 2037 ATTCTAATTAATTC 2048

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RESULT 5
AAA37963
ID AAA37963 standard; DNA; 2048 BP.

XX AAA37963;
AC
XX
DT 18-AUG-2000 (first entry)
XX
XX plasmid #2 DNA sequence used in mutation of promoter sequence.
DE
XX Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds.
XX
XX Daucus carota.
OS
XX
XX
XX MO200020613-A1.
PN
XX
XX 13-APR-2000.
PD
XX
XX 28-SEP-1999; 99MO-JP005303.
PP
XX
XX 02-OCT-1998; 98JP-00281124.
PR
XX
XX (SUMO) SUMITOMO CHEM CO LTD.
PA
XX
XX Nishikawa S, Oeda K;
PI
XX
XX WPI; 2000-303791/26.
DR
XX
XX
XX New Plant promoters and terminators from Daucus carota L., useful in
PT plant breeding, for e.g. controlling fertilities of plants.
XX
XX
XX Example 8; Page 73-74; 81pp; English.
PS
XX
XX This sequence represents a plasmid sequence used in a method for
CC introducing a mutation into a carrot promoter. The invention relates to
CC plant promoters and terminators from Daucus carota L. which are capable of
CC expressing a gene of interest in plants. The invention also includes a
CC chimeric gene characterized in that it comprises the promoter and a
CC desired gene linked to each other in the form capable of functioning. A
CC method of producing a transformant comprises introducing the promoter,
CC the chimeric gene or a vector comprising the promoter and a desired gene
CC or terminator sequence into a host cell. The plant promoters and
CC terminators are useful in plant breeding, for e.g. fertilities of plants
CC may be controlled by expressing, in the host cells, a sense or antisense
CC gene of a male sterility related gene such as S-locus-specific Rase gene
CC
XX
SQ Sequence 2048 BP; 735 A; 317 C; 316 G; 680 T; 0 U; 0 Other;
Query Match 99.0%; Score 2030.8; DB 3; Length 2048;
Best Local Similarity 99.7%; Pired. No. 0;
Matches 2046; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 1 CATGTCGCTTACGACACATAGGCGCTGTTGGTTGAGAGACGAAAGCTCTTGA 60
DB 1 CATGTCGCTTACGACACATAGGCGCTGTTGGTTGAGAGACGAAAGCTCTTGA 60
QY 61 CTTCCTCTCTTCTTGAAGCTGTTGTATTAAGAAGTGAATATTTTAAAGAGCTCGAA 120
DB 61 CTTCCTCTCTTCTTGAAGCTGTTGTATTAAGAAGTGAATATTTTAAAGAGCTCGAA 120
QY 121 TACTTAACCTCTCTCAACCTCCGCTCTTTTCCAAACACTTATTAATTTTAACT 180
DB 121 TACTTAACCTCTCTCAACCTCCGCTCTTTTCCAAACACTTATTAATTTTAACT 180
QY 181 TCTCATTTTACACGCTCTTGTGCTATAGCAAGAAATCACTCTTTTAAGTAACTCA 240
DB 181 TCTCATTTTACACGCTCTTGTGCTATAGCAAGAAATCACTCTTTTAAGTAACTCA 240
QY 241 AACGCGCTCAATTAAGATCATTAATATGATCTTTCAATTTTGAATTAACATACGT 300
DB 241 AACGCGCTCAATTAAGATCATTAATATGATCTTTCAATTTTGAATTAACATACGT 300
QY 301 GAACAGGCTTATTTTAAAGCTGCAACAATTTAATAATTTTAACTGCGCGGTGAAC 360
DB 301 GAACAGGCTTATTTTAAAGCTGCAACAATTTAATAATTTTAACTGCGCGGTGAAC 360

QY 361 CCGTCTTCCAGATAATATATTTTAAATTTGTAGACCTCCCTTTTAAACCAATTCGATGC 420
DB 361 CCGTCTTCCAGATAATATATTTTAAATTTGTAGACCTCCCTTTTAAACCAATTC---GC 416
QY 421 AGAGACATTTAGGTGAATACACTTGTACTGTGAGCTTTTAAACAAAGAAAGTGTTC 480
DB 417 AGAGACATTTAGGTGAATACACTTGTACTGTGAGCTTTTAAACAAAGAAAGTGTTC 476
QY 481 ATGCTAGGCATCAAAATTTGACAAACCCGACCAACACTCTATGACGACTATCTTT 540
DB 477 ATGCTAGGCATCAAAATTTGACAAACCCGACCAACACTCTATGACGACTATCTTT 536
QY 541 TGCGCGAATGCTTCTCAAAATGTTTTTATATGTAATTAATATCCATCCAAAGATTAAGT 600
DB 537 TGCGCGAATGCTTCTCAAAATGTTTTTATATGTAATTAATATCCATCCAAAGATTAAGT 596
QY 601 AAAATCCCGTTTAAACGAGTTGTTATATATATGTTTACACTTACAGAGATATTCGT 660
DB 597 AAAATCCCGTTTAAACGAGTTGTTATATATATGTTTACACTTACAGAGATATTCGT 656
QY 661 AATACCTTTAGACGACAGAGACTTAGTCAAAAATGAGACGCTGTTAAACAGCTAGACT 720
DB 657 AATACCTTTAGACGACAGAGACTTAGTCAAAAATGAGACGCTGTTAAACAGCTAGACT 716
QY 721 TGCTCATGATTAATAGATTAATGTTAGTATATATATAGATCTTACATGACATTTAA 780
DB 717 TGCTCATGATTAATAGATTAATGTTAGTATATATATAGATCTTACATGACATTTAA 776
QY 781 ATTAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
DB 777 ATTAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 836
QY 841 AAAACAGAGCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 837 AAAACAGAGCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
QY 901 TAACTGATCTAAGACATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
DB 897 TAACTGATCTAAGACATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 956
QY 961 TTAACGAAATCAATTTTAAACATGCTCTGCGCTGCTCAATTAATTAATTAATTAATTAAT 1020
DB 957 TTAACGAAATCAATTTTAAACATGCTCTGCGCTGCTCAATTAATTAATTAATTAATTAAT 1016
QY 1021 TGATCATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
DB 1017 TGATCATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1076
QY 1081 AAGAAGACATGCTCTCTTGAAGAAACAAATTAATTAATTAATTAATTAATTAATTAATTA 1140
DB 1077 AAGAAGACATGCTCTCTTGAAGAAACAAATTAATTAATTAATTAATTAATTAATTAATTA 1136
QY 1141 ATACATATGATTTGACACGAGACCTAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1200
DB 1137 ATACATATGATTTGACACGAGACCTAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1196
QY 1201 AAAAGAGAGAAAGTGGGTAAAGTACCGGACCCCAATATATTAATTAATTAATTAATTAAT 1260
DB 1197 AAAAGAGAGAAAGTGGGTAAAGTACCGGACCCCAATATATTAATTAATTAATTAATTAAT 1256
QY 1261 AAAAGTATGTAAGTATGAGTGGGTGGGATTTTATATTAATTAATTAATTAATTAATTAAT 1320
DB 1257 AAAAGTATGTAAGTATGAGTGGGTGGGATTTTATATTAATTAATTAATTAATTAATTAAT 1316
QY 1321 AGAAGTATGTAAGTATGAGTGGGACATCAATAAGAGAAAGTATTAATTAATTAATTAAT 1380
DB 1317 AGAAGTATGTAAGTATGAGTGGGACATCAATAAGAGAAAGTATTAATTAATTAATTAATTAAT 1376
QY 1381 TAAATGGGACAGAGGAGTAAATCTTATATATTAATTAATTAATTAATTAATTAATTAATTA 1440
DB 1377 TAAATGGGACAGAGGAGTAAATCTTATATATTAATTAATTAATTAATTAATTAATTAATTA 1436
QY 1441 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500

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RESULT 6
AAV15144
ID AAV15144 standard; DNA; 2042 BP.
XX
AC AAV15144;
XX
XX
DT 02-JUL-1998 (first entry)
XX
DE New promoter used for root-specific expression in plants.
XX
KW Promoter; root; carrot; Xuroda Gosun; root-specific expression;
KW plant cell; soil pathogen; improve; nutritive value; edible root plant;
XX ss.
XX
OS Daucus carota.
OS
XX
PN EP824150-A2.
XX
PD 18-FEB-1998.
XX
PF 12-AUG-1997; 97EP-00113923.
XX
PR 12-AUG-1996; 96UP-00212680.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI Torikai S, Oeda K;
XX
WPI; 1998-122310/12.
DR

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| Query | Sequence | 2042 BP | 719 A | 356 C | 323 G | 644 T | 0 U | 0 Other |
|-----------------------|----------|---|-------------------|----------|-------------|-------|-----|---------|
| Query Match | | 11.7% | Score 239.6 | DB 2 | Length 2042 | | | |
| Best Local Similarity | | 72.6% | Pred. No. 8.7e-35 | | | | | |
| Matches 366 | | Conservative 0 | Mismatches 129 | Indels 9 | Gaps 4 | | | |
| QY | 1554 | AAATCGATTTCTGAAAAGCAATATATCTTTGTGTAACACGCG---TTGGTGCAATNG | 1602 | | | | | |
| DB | 1543 | AAATTTATTTATCTGAATGATTAACATCTTTGTAAACAAACGCGCAATAGACCATPA | 1602 | | | | | |
| QY | 1610 | GGAAGTTCATNGTGATTCATATGTTTAAATATAAAGTAATTTAAATTAATGTTAAT | 1668 | | | | | |
| DB | 1603 | CGAAGTTCAAGGTATCTTTAAATGTATATCAATGACATGAGATTTTCTT--TTCAAGT | 1666 | | | | | |
| QY | 1670 | TTTGTTTCAGAAATTTAAATTAATTAATTAATGACATGGAGGTCACGGGCATCAFTAGC | 1729 | | | | | |
| DB | 1661 | ATPAAGTTATTTCTTCATCAATCAATTAACCTTTAAATTTGACATTAATGACAACTTATAGCC | 1720 | | | | | |
| QY | 1730 | AGCAGTACAGCTTTTGAAACAAATGATATGCGGTGTACATCTATAGACCTTTCAACTCAAC | 1789 | | | | | |
| DB | 1721 | CAGGTGATATGTTTAAACAAAGCTTTGTGCGGTATATATTAATTAACCTTTCAACTCAAGC | 1780 | | | | | |
| QY | 1790 | TATGTAAAT-AATGCACTTGTAGAATACATCTTTTCAAAATTTCAACAACACAGCTTAAT | 1848 | | | | | |
| DB | 1781 | TAGCCAGGAATGCTTTCTAGAAATATATCTTTGAATTTCAACAAACACAGCACTRACT | 1840 | | | | | |
| QY | 1849 | TTTCTTTCAAGGATTTGGAATCCCTTTCTTAACTTTTAAATTAATAAATAATCATTAAT | 1908 | | | | | |
| DB | 1841 | TTTCTTTTAAAGATTTGAATCGTTTGTGTAACCTTTTAAATTT--AAAAATCATTAAT | 1898 | | | | | |
| QY | 1909 | GTAATATTTTCAACACCTTACATTTGATGTAGTACGTACTATATAATAGGCGCTTGATG | 1968 | | | | | |
| DB | 1899 | ATAATATTTTCAACACCTTCAACATTCATGTAGCGTACATATTAATAGGTGCTCTTGATG | 1958 | | | | | |
| QY | 1969 | CTCTACTATCATCAACATCAATCTTAAACCAACAACTTGAAGCTTAAATTTTCTACTTAAT | 2028 | | | | | |
| DB | 1959 | CTCTACTATCATCAACATCAATCTTCAAGCAACAACTTGAAGCTTAAATCTTCTACTATAT | 2018 | | | | | |
| QY | 2029 | CTAGCAATATCAATCTTAAATATC | 2052 | | | | | |
| DB | 2019 | TTTAGCAAAAACATTTCTAAAGGTC | 2042 | | | | | |

| | |
|----------|---|
| RESULT 7 | |
| AAV15143 | |
| ID | AAV15143 standard; DNA, 247 BP. |
| XX | |
| AC | AAV15143; |
| XX | |
| DT | 02-JUL-1998 (first entry) |
| XX | |
| DE | New promoter used for root-specific expression in plants. |
| XX | |
| KM | Promoter; root; carrot; Kuroda Gosun; root-specific expression; |
| KM | plant cell; soil pathogen; improve; nutritive value; edible root plant; |
| XX | ss. |
| XX | |
| OS | Daucus carota. |
| XX | |

PN EP824150-A2.
XX
PD 18-FEB-1998.
XX
PF 12-AUG-1997; 97EP-00113923.
XX
PR 12-AUG-1996; 96JP-00212680.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Torikata S, Oeda K;
XX
DR WPI; 1998-122310/12.
XX
PT New carrot root gene, promoter and terminator - useful in genetic
PT engineering for directing root-specific gene expression.
XX
PS Claim 1; Page 14; 31pp; English.
XX
CC The present sequence represents a novel promoter, and is isolated from
CC the roots of carrots, cultivar Kuroda Goshun. The promoter can be used to
CC direct root-specific expression in plant cells. Since the promoter
CC enables expression of a desired protein in the roots of a plant, it is
CC useful in combat against pathogenic soil fungi and pests which are
CC difficult to kill by chemicals. It can also be used to improve the
CC nutritive value of edible root plants
XX
SQ Sequence 247 BP; 88 A; 50 C; 21 G; 88 T; 0 U; 0 Other;

Query Match 9.6%; Score 196.6; DB 2; Length 247;
Best Local Similarity 89.6%; Pred. No. 5.8e-27;
Matches 223; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 1804 TTCTAGAAATACATCTTTTCAAAATTTCAACAAACAGCTTAACTTTCTTTCAACGGAT 1863
DB 1 TTCTAGAAATACATCTTTTGAATTTCAACAAACAGCTAACTTTCTTTAAACAGAT 60
QY 1864 TGAATCCTTTCTAACTTTTAAATATAAATAAATGATATTGTAATATTATCAAC 1923
DB 61 TGAATCCTTTCTAACTTTTAAATTT--AAAAATACATTACTAATATTATTTATCAAC 118
QY 1924 ACCTCAACATTGATGTTAGCGTACTAATAATAGTGCTCTTGCTCTACTATCATCAAC 1983
DB 119 ACCTCAACATTGATGTTAGCGTACTAATAATAGTGCTCTTGCTCTACTATCATCAAC 178
QY 1984 ATCAATCTTACACCAAAACCTTGAGCTTAATTTTCTACTTATCTCAGCAATTAACATT 2043
DB 179 ATCAATCTTCCAGCAAAACCTTGAGCTTAATCTTCTACTAATTTTGACAAAAACATT 238
QY 2044 CTTAAATATC 2052
DB 239 CTTAAAGCTC 247

RESULT 8
AAZ49611
ID AAZ49611 standard; DNA; 246 BP.

AC AAZ49611;
XX
DT 07-APR-2000 (first entry)
XX

DE Carrot CR16.3 fragment for synthesis of plant promoter.

XX
KW Synthetic DNA; plant promoter; CR16.3 fragment; carrot; transgenic plant;
KW soybean glycinin; stearyl-ACP-desaturase gene;
KW male sterility-related gene; ds.
XX

OS Daucus carota.
XX
PN EP976833-A2.
XX
PD 02-FEB-2000.

XX
XX 13-JUL-1999; 99EP-00113732.
XX
XX 15-JUL-1998; 98JP-00200372.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Iehige F, Nishikawa S, Oeda K;
XX
DR WPI; 2000-128374/12.
XX
PT Novel promoter used to produce transgenic plants with higher expression
PT of a desired gene.
XX
PS Claim 1; Page 11-12; 24pp; English.

CC The present sequence is a CR16.3 fragment from carrot genomic DNA. It is
CC used for synthesis of a plant promoter which comprises nucleotides 112-
CC 246, 54-246, or 1-246 of this sequence and a synthetic DNA. The promoter
CC is used for controlling the expression of a desired gene e.g. soybean
CC glycinin, stearyl-ACP-desaturase and S-locus type specific RNase gene
CC (male sterility-related gene) in a host cell especially a microorganism
CC or a plant cell. The transformed plant cells can be used to produce
CC transgenic plants. The promoter is compact and therefore suitable for
CC higher expression of a desired gene in a particular tissue compared to
CC other host tissues
XX
SQ Sequence 246 BP; 88 A; 50 C; 21 G; 87 T; 0 U; 0 Other;

Query Match 9.5%; Score 195.6; DB 3; Length 246;
Best Local Similarity 89.5%; Pred. No. 8.9e-27;
Matches 222; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 1805 TCTAGAAATACATCTTTTCAAAATTTCAACAAACAGCTTAACTTTCTTTCAACGGATT 1864
DB 1 TCTAGAAATACATCTTTTGAATTTCAACAAACAGCTAACTTTCTTTAAACAGATT 60
QY 1865 GGAATCCTTTCTAACTTTTAAATATAAATAAATGATATTGTAATATTATCAAC 1924
DB 61 AGAATCCTTTCTAACTTTTAAATTT--AAAAATACATTACTAATATTATTTATCAAC 118
QY 1925 CCTCAACATTGATGTTAGCGTACTAATAATAGTGCTCTTGCTCTACTATCATCAAC 1984
DB 119 CCTCAACATTGATGTTAGCGTACTAATAATAGTGCTCTTGCTCTACTATCATCAAC 178
QY 1985 TCAATCTTACACCAAAACCTTGAGCTTAATTTTCTACTTATCTCAGCAATTAACATT 2044
DB 179 TCAATCTTCCAGCAAAACCTTGAGCTTAATCTTCTACTAATTTTGACAAAAACATT 238
QY 2045 TAAATATC 2052
DB 239 TAAAGGTC 246

RESULT 9
ADP07499
ID ADP07499 standard; DNA; 196 BP.

AC ADP07499;
XX
DT 29-JUL-2004 (first entry)
XX

DE Carrot DNA.

XX
KW Carrot; gene; ds; expression inducing promoter;
KW transcription start point; RNA polymerase II.
XX

OS Daucus carota.
XX
PN JP2004135597-A.
XX
PD 13-MAY-2004.

promoter. Specifically, it refers to promoter sequences derived from plant DNA, preferably carrot and functional in carrot cells.

CC used as expression inducers. Furthermore, the present invention describes
CC DNA, vectors, transformants and the process by which to prepare
CC transformants. This polynucleotide sequence is DNA encoding a carrot
CC promoter (segid 3) of the invention.

XX Sequence 2865 BP; 963 A; 461 C; 396 G; 1045 T; 0 U; 0 Other;

Query Match 7.9%; Score 162.4; DB 10; Length 2865;
Best Local Similarity 82.5%; Pred. No. 1.5e-20;
Matches 198; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 22 AGGCGCTGTTTGGTGAAGAAAGCAAGCTGCTTGACTTCTTCTTTGACCTGT 81

DB 1716 AGGGCGCTGTTTGTATGAAATCAGAAAGCTGCTTGACTTCTGTTTTTTT -ACCGGT 1774

QY 82 TTGTATTAAGAAGTAAATATTTTAAAAAGCTGGAGTACTTCTCTCTCAAC 141

DB 1775 TTGTGTAAAAAGAGAACACTTTTAAAGAGCTGAGAAATGCTTCTCTCTCAAC 1834

QY 142 TTCCGCTTCTTCCAAACACTTTTATTAATCTTCTTCTTCTTCTTCTTCTTCT 201

DB 1835 TTCTGCTTCTTCTTCCAAACACTTTTATTAATCTTCTTCTTCTTCTTCTTCTTCT 1894

QY 202 TTGCTATTAAGCAAGAAATCACTTCTTTAAGCTAACCCAAAGGCTCTAATTAAGATCA 261

DB 1895 TTACTATTAAGCAAGAAATCACTTCTTTAATTAATTAACCCAAAGGCTCTAATTAATTTGA 1954

RESULT 12
AAZ49616/C

ID AAZ49616 standard; DNA; 140 BP.

XX AAZ49616;

DT 07-APR-2000 (first entry)

XX Oligonucleotide-4 for synthesis of CR16.1 fragment for plant promoter.

DE Synthetic DNA; plant promoter; CR16.1 fragment; carrot; transgenic plant;

KM soybean glycinin; oligonucleotide; stearyl-ACP-desaturase gene;

KW male sterility-related gene; ss.

XX Daucus carota.

OS Synthetic.

XX EP976832-A2.

PD 02-FEB-2000.

PF 13-JUL-1999; 99EP-00113732.

PR 15-JUL-1998; 98UP-00200372.

PA (SUMO) SUMITOMO CHEM CO LTD.

PI Ishige F, Nishikawa S, Oeda K;

PT Novel promoter used to produce transgenic plants with higher expression

XX of a desired gene.

XX Disclosure; Page 14; 24pp; English.

XX The present sequence is an oligonucleotide (- chain) used to prepare a

CC CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3

CC fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for

CC construction of a plant promoter. The promoter is used for controlling

CC the expression of a desired gene e.g. soybean glycinin, stearyl-ACP-

CC desaturase and S-locus type specific RNase gene (male sterility-related

CC gene) in a host cell especially a microorganism or a plant cell. The

CC transformed plant cells can be used to produce transgenic plants. The

CC promoter is compact and therefore suitable for higher expression of a

CC desired gene in a particular tissue compared to other host tissues

XX Sequence 140 BP; 45 A; 17 C; 34 G; 44 T; 0 U; 0 Other;

Query Match 5.8%; Score 119; DB 3; Length 140;

Best Local Similarity 92.6%; Pred. No. 1.1e-12;

Matches 125; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1918 ATCAACACCTGAACATTTGATGTTAGGCTATTAATAGTGTCTGTGGTCTACTAT 1977

DB 140 ATCAACACCTGAACATTTGATGTTAGGCTATTAATAGTGTCTGTGGTCTACTAT 81

QY 1978 CATCAATCAATCTTACACCAACCTTGAAGCTTAATTTTCTACTTATTCAGCAAT 2037

DB 80 CATCAATCAATCTTCCAGCAACAACTTGAGCTTAATCTTCTACTAATTTTTCAGCA 21

QY 2038 AACATTTCTAATATC 2052

DB 20 AACATTTCTAAGTTC 6

RESULT 13
AAZ49615

ID AAZ49615 standard; DNA; 140 BP.

XX AAZ49615;

DT 07-APR-2000 (first entry)

XX Oligonucleotide-3 for synthesis of CR16.1 fragment for plant promoter.

DE Synthetic DNA; plant promoter; CR16.1 fragment; carrot; transgenic plant;

KM soybean glycinin; oligonucleotide; stearyl-ACP-desaturase gene;

KW male sterility-related gene; ss.

XX Daucus carota.

OS Synthetic.

XX EP976832-A2.

PD 02-FEB-2000.

PF 13-JUL-1999; 99EP-00113732.

PR 15-JUL-1998; 98UP-00200372.

PA (SUMO) SUMITOMO CHEM CO LTD.

PI Ishige F, Nishikawa S, Oeda K;

PT Novel promoter used to produce transgenic plants with higher expression

XX of a desired gene.

XX Disclosure; Page 13; 24pp; English.

XX The present sequence is an oligonucleotide (+ chain) used to prepare a

CC CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3

CC fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for

CC construction of a plant promoter. The promoter is used for controlling

CC the expression of a desired gene e.g. soybean glycinin, stearyl-ACP-

CC desaturase and S-locus type specific RNase gene (male sterility-related

CC gene) in a host cell especially a microorganism or a plant cell. The

CC transformed plant cells can be used to produce transgenic plants. The

CC promoter is compact and therefore suitable for higher expression of a

QY 1918 ATCAACAGCTCAACATTAATGTTAGCGTACTATAATAGTGTCTTGGTCTTACTAT 1977
 DB 5 ATCAACAGCTCAACATTAATGTTAGCGTACTATAATAGTGTCTTGGTCTTACTAT 64
 QY 1978 CATCAATCAATCTTACGACGACAAACCTGAGCTTAATTTTCTACTTATTTGACCAAT 2037
 DB 65 CATCAATCAATCTTACGACGACAAACCTGAGCTTAATTTTCTACTTATTTTACCAAA 124
 QY 2038 AACATTTCTAAATATATC 2052
 DB 125 AACATTTCTAAAGGTC 139

RESULT 14
 ABZ10246
 ID ABZ10246 standard; DNA, 8056 BP.
 XX
 AC ABZ10246;
 XX
 DT 16-JAN-2003 (first entry)
 XX

De Haematopoietic cell proliferation disorder related DNA sequence #386.

XX Human: haematopoietic cell proliferation disorder; cytosratic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; ds.
 XX

OS Homo sapiens.

PN MO20027272-A2.

PD 03-OCT-2002.

PF 26-MAR-2002; 2002WO-EP003401.

PR 26-MAR-2001; 2001US-0278333P.

PA (EPIC-) EPIGENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
 PI Lewin A, Lipschitz B, Mater S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwope I, Ziebarth H;
 XX WPI; 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX

PS Claim 28; SEQ ID NO 386; 117bp; English.

XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subtypes, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a

CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 XX Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 4.8%; Score 99.4; DB 8; Length 8056;
 Matches 624; Conservative 0; Mismatches 761; Indels 18; Gaps 5;

QY 548 ATGCTCTCAAAATGTTTTTATATGTAATTAATAGCCATCAAGTAACTAAATTC 607
 DB 1975 ATTAATATTAATTTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2034
 QY 608 CCGTTTACCAAGTTGTTAATATATATGTTTACCTTACAGAGATATGTAATCTT 667
 DB 2035 ATTTTAAATATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2094
 QY 668 TTAGACGACAGAGAGTACGTCACAAATGACGCTGTAAACAGCTTACCTGTCAC 727
 DB 2095 AATTAATTAATTAATTTTATTAATTAATTAATTTTAAATTTTAAATTTTAAATTA 2154
 QY 728 TGATTAATATGATTAATGTTAGTATATATAGTATGATCTACATGACATTAATTAAG 787
 DB 2155 TAAAAAATTAATTAATTTTATTAATTTTAAATTTTAAATTTTAAATTTTAAATTA 2214
 QY 788 CTATTAATTAAGTTACTAATTAATTAAGAGGTTAGTAACAGAAACAGGTAAACAA 847
 DB 2215 AAAAAAATTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTA 2274
 QY 848 GAGCTTGCTGCTGTGTGTTAGTTGTGTGAGCTCATTC-----TTTAAAGTATATG 901
 DB 2275 AATTTTAAATTTTAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2334
 QY 902 AAACGTATCTAAACAGATTAATTTAGTACAGGTTAAACCTTTTACAGAAATTAAT 961
 DB 2335 AATTTTATTAATTTTAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2394
 QY 962 TAAAGAAATCATTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAA 1021
 DB 2395 TATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2451
 QY 1022 GATCATCATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1081
 DB 2452 TTATTTTATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2511
 QY 1082 AGAAGCAATATGCTCTTTGAAAAAACAATATGTAATCCCTCCGCTCGAAATGTA 1141
 DB 2512 AATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 2571
 QY 1142 TACATATGATTTGACAGGACGACGTAAGAAATGTAATTAATTAATTAATTAATTAATTA 1201
 DB 2572 TTTTAAAAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 2631
 QY 1202 AAGAGAAAGAAAGTGGTAAAGTACGCGGACCCACCAATTAATTAATTAATTAATTAAG 1261
 DB 2632 AAAAAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2691
 QY 1262 AAGATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1321
 DB 2692 TAAATTTTATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 1381
 QY 1322 GAAAGTTTGAATGTAATTAATTAATTTGAGGACATCCATTAATTAATTAATTAATTAATTA 1381
 DB 2748 AAAAAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 2807
 QY 1382 AATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1441
 DB 2808 AATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2865
 QY 1442 AAGATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1501
 DB 2866 TTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 2925

QY 1502 TGATTAGCATTCACCGCCTTTTATATTTTACATACAGTAATATGTAATATATCAGT 1561
DB 2926 AATTATTAATGAAATGTAATATTTTAAATGAAATTAATATTTGTTAAAAAATAAAAAAATTA 2985
QY 1562 TATCGAAAAAGCAATATATCTTTGTAAACAGCGTTGGTCAAAATGGAGTTGATGT 1621
DB 2986 TTGAAAAAATGATATATTTTAAATATGATGATTTTAAATTTATTAATTAATTAATAA 3045
QY 1622 GATTCATAGATTTTAAATTAATAAGTAATTTTAAATTAATTTGTTTGTTCAGAA 1681
DB 3046 TAAATTAATATGTTATATATGTAATGAAATTTGAATTAATTTGTTATATGTAATTT 3105
QY 1682 ATTAAATTAATTAATTTGAGCATGAGAGTTCCAGGCAATTTGAGCAGCATAGACTG 1741
DB 3106 AATTAATAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3165
QY 1742 ---TTTGAACAATGATATGTCGGGTGATCATATGACCTTTCAACTCAACTAGTGAATA 1798
DB 3166 AATTTTAAATTAATTAATTTTAAATTTTAAATTTTGTGTTGTAATTTGTAATTAATTTT 3225
QY 1799 ATGCATCTAGAAATCATCTTTTCAAATTTCAACAACAGCTTAACTTTCTTCAA 1858
DB 3226 AATTATTAATTAATTTTAAATTAATTTGATTAATTTTAAATTAATTTGATTTGTAATA 3285
QY 1859 CGAATGGAATCCTTTCTTAACTTTTAAATTAATAAATGATTTATTTGTAATTTTA 1918
DB 3286 AATTTTGTATTTGTTGTTGTTATTTTGTGAAAAAATAATTAATTTGTAATTTAA 3345
QY 1919 TCACACCTCAACATTTGATGTTA 1941
DB 3346 AAAATGAATTAATTAATTTGAATGA 3368

RESULT 15

ABZ10100 standard; DNA; 8056 BP.

ABZ10100;

16-JAN-2003 (first entry)

Haematopoietic cell proliferation disorder related DNA sequence #240.

Human; haematopoietic cell proliferation disorder; cytostatic;

KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KM cytosine methylation state; gene; ds.

Homo sapiens.

WO00272722-A2.

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P.

(EPIC-) EPIGENOMICS AG.

Berlin K, Braun A, Disler J, Guetig D, Howe A, Mueller J;

PI Lewin A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;

PI Schwope I, Ziebach H;

MPI, 2003-018942/01.

detecting and differentiating between hematopoietic cell proliferative

disorders, comprises contacting a target nucleic acid with a reagent that

distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 28; SEQ ID NO 240; 117bp; English.

The present invention describes a method for detecting and

CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients

Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match 4.5%; Score 91.8; DB 8; Length 8056;
Best Local Similarity 44.2%; Pred. No. 1.8e-07;
Matches 627; Conservative 0; Mismatches 767; Indels 25; Gaps 5;

QY 547 AATGCTTCAAAATGTTTATATATGTAATTAATATCCATCCAGATGAATTAAT 606
DB 1358 AATTTTATTAATAAATTTATTTTATTAATAAATATGCAATTTTATTTTATTTT 1417
QY 607 CCCGTTAACAGTTGTTATATATATGTTTACCTTCAAGAGATTTGTAATCT 666
DB 1418 TTTATTTTATTTTATTAATAAATAAATAATTAATTTTATTAATAATTAATAA 1477
QY 667 TTTAGACGACAGAGACTAGCTCAAAATGACGCTGTAAACAGCTTGAATTTG 726
DB 1478 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1537
QY 727 CTGATTAATGATTAATTTGTTATTAATTAATTAATTAATTAATTAATTAATTA 786
DB 1538 TTAATAAATAATTTTATTTTATTAATAATTAATTAATTTTATTTATTTATTTA 1597
QY 787 GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 846
DB 1598 TAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 1657
QY 847 AGAGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 906
DB 1658 AATTATTAATTAATTTTATTTTATTAATAATTAATAATTAATTAATTAATTA 1716
QY 907 GATCTTAAGCAGATGAATAATTTAGTACAGTTTAACTTTTACAGAAATTTATTTAA 966
DB 1717 TATATATTAATTAATTTTATTTTATTAATAAATAAATAAATAATTTTATTTAA 1776
QY 967 GAAATCATTTTATTAATCATGCTCTCGGCTGATTTATTAATGAGGATCACTTAC 1026
DB 1777 AATTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1836
QY 1027 TCCATTAATAAATTTGTTAAACAAATTTCAATGAGATTAATTTTCAATGAAAGA 1086
DB 1837 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1896
QY 1087 GACAAATGCTCTTTGAAAAAACAATAAGTACTCCCTCGCTCTGAATGTATACAT 1146
DB 1897 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1956
QY 1147 ATGCAATGACACGAGACTAAGAAATATGTTAAAGTATGATAGTAAAGAAAGAG 1206
DB 1957 AATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2016
QY 1207 A-----AAGAAAGTGGGTAAAGTAAAGGAGCAACCAATATATTAATTAAT 1256

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 08:19:54 ; Search time 6529.36 Seconds
(without alignments)
11962.561 Million cell updates/sec

Title: US-09-806-197-1

Perfect score: 2052
Sequence: 1 catgtcgtgcctcacagcaca.....gcaatacatcttaataatc 2052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| C 1 | 97.8 | 4.8 | 1101 | 9 | CNS00EVL |
| C 2 | 97.2 | 4.7 | 1101 | 9 | AL069706 Drosophila |
| C 3 | 95.6 | 4.7 | 1542 | 9 | AG386981 Mus muscu |
| C 4 | 95 | 4.6 | 1101 | 9 | CNS0039G |
| C 5 | 94.6 | 4.6 | 1758 | 9 | AL069921 Drosophila |
| C 6 | 93.6 | 4.6 | 1896 | 9 | CL509408 SAHL 811 |
| C 7 | 93 | 4.5 | 1202 | 8 | CG753083 P048-1-CO |
| C 8 | 92.4 | 4.5 | 1101 | 9 | CC262481 CH261-167 |
| C 9 | 90.8 | 4.4 | 1101 | 9 | AL061936 Drosophila |
| C 10 | 90.4 | 4.4 | 1608 | 9 | AL069706 Drosophila |
| C 11 | 88.8 | 4.3 | 1067 | 6 | CL118721 ISB1-7208 |
| C 12 | 88.8 | 4.3 | 1268 | 9 | CD386564 AGENCOURT |
| C 13 | 88.8 | 4.3 | 1392 | 9 | AG347098 Mus muscu |
| C 14 | 88 | 4.3 | 1277 | 8 | CG757503 P052-4-CO |
| C 15 | 88 | 4.3 | 1277 | 8 | CC255231 CH261-180 |
| C 16 | 87.6 | 4.3 | 1696 | 9 | AG346840 Mus muscu |
| C 17 | 87.2 | 4.2 | 1275 | 9 | CL033318 CH216-36F |
| C 18 | 87 | 4.2 | 187 | 9 | AG526041 Mus muscu |
| C 19 | 87 | 4.2 | 1275 | 9 | AG526041 Mus muscu |
| C 20 | 86.8 | 4.2 | 2087 | 9 | CL033318 CH216-36F |
| C 21 | 85.6 | 4.2 | 1350 | 9 | CG749499 P043-4-AO |
| C 22 | 85.4 | 4.2 | 1780 | 9 | CL019486 CH216-5G1 |
| C 23 | 85.2 | 4.2 | 1320 | 9 | AG320553 Mus muscu |
| C 24 | 85 | 4.1 | 1539 | 9 | CL103881 ISB1-42C8 |
| | | | | | AG340947 Mus muscu |

| | | | | | |
|------|------|-----|------|---|---------------------|
| C 25 | 84.8 | 4.1 | 1254 | 9 | AG349719 Mus muscu |
| C 26 | 84.6 | 4.1 | 987 | 9 | AL104456 Drosophila |
| C 27 | 84.6 | 4.1 | 1364 | 9 | CG757970 P053-2-CO |
| C 28 | 84 | 4.1 | 1101 | 9 | AL108152 Drosophila |
| C 29 | 83.8 | 4.1 | 822 | 7 | CK416977 AUF_IPint |
| C 30 | 83.6 | 4.1 | 1489 | 9 | AG350139 Mus muscu |
| C 31 | 83.4 | 4.1 | 1101 | 9 | AL070972 Drosophila |
| C 32 | 83 | 4.0 | 1211 | 9 | AG349657 Mus muscu |
| C 33 | 83 | 4.0 | 1592 | 9 | CG750135 P044-3-DO |
| C 34 | 82.8 | 4.0 | 1210 | 9 | CG749728 P044-1-CO |
| C 35 | 82.6 | 4.0 | 1506 | 9 | AG278469 Mus muscu |
| C 36 | 81.6 | 4.0 | 1092 | 9 | AL175696 tetradon |
| C 37 | 81.6 | 4.0 | 1101 | 9 | CNS00E07 |
| C 38 | 81.6 | 4.0 | 1355 | 9 | AG346348 Mus muscu |
| C 39 | 81.6 | 4.0 | 1745 | 9 | AG338221 Mus muscu |
| C 40 | 81.4 | 4.0 | 812 | 8 | BH178455 011_J_02- |
| C 41 | 81.4 | 4.0 | 812 | 9 | CNS07KSM |
| C 42 | 81.4 | 4.0 | 1050 | 9 | CNS01JMS |
| C 43 | 81.4 | 4.0 | 1391 | 9 | CG754863 P050-2-GO |
| C 44 | 81.2 | 4.0 | 1094 | 9 | CNS012F2 |
| C 45 | 81.2 | 4.0 | 1715 | 9 | AG288305 Mus muscu |

ALIGNMENTS

RESULT 1
CNS00EVL/C 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29823 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL069706.1 GI:4949849
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pletier de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source 1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_1fb="RPCI-98"
/note="end : T7"

ORIGIN

Query Match 4.8%; Score 97.8; DB 9; Length 1101;
Best Local Similarity 34.8%; Pred. No. 8.7e-08;

AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 TITLE BAC end Sequences of Library MSWg01
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1542)
 AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (17-NOV-2003) Masahito Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shuhiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 COMMENT Clones are derived from the mouse BAC library MSWg01. For BAC library availability, please contact Kunihya Abe (abe@rc.riken.jp).
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY : PBACg3.6
 Vector : Ecoli
 R.Site 1 : Ecoli
 R.Site 2 : Ecoli.
 FEATURES
 source
 1. 1542
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSWg01-201G10.TJ"
 /sex="male"
 /issue_type="mixture of kidney and spleen"
 /clone_lib="MSWg01 Mouse Male BAC library"

Query Match 4.7%; Score 95.6; DB 9; Length 1542;
 Best Local Similarity 44.3%; Pred. No. 2.2e-07;
 Matches 420; Conservative 0; Mismatches 523; Indels 6; Gaps 1;

QY 750 ATATATAGTAGTACATGACATTAATTAAGCTATTAAATTAAGTTAACTAATA 809
 |||||
 DB 1103 ATATAGAAATTTAT 1044
 QY 810 ATTAAGAGAGTTAGTAAAGAAAGAGAGTTAAAGCAAGCTGCTGCTGCTTTAG 869
 |||||
 DB 1043 AAT 984
 QY 870 TTGTTGTGAGCTCTTTTAAAGTAAATGTAATCTAATGACATAGAAATTTA 929
 |||||
 DB 983 TTTAT 924
 QY 930 GTACAGGTTAAACCTTTTCAAGAAATTTATTTAAAGAAATCATTTTATACATGCT 989
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 DB 923 ATTAAT 864
 QY 990 CTCGGCTGCTATATATATGCGATCTTATGATCATCCATTA-----AACCTTGT 1043
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 DB 803 AAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 744
 QY 1104 AAAACAAATAGTACTCCCTCCCTCCCTGTAATGTATATACATATGATTTGACACGAG 1163
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 DB 743 TAAAT 684
 QY 1164 ACTAAGAAAAATGTATTAAGTATATAGGTAAAAAGAAAGCAAGAAAGTGGTAAA 1223
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 DB 683 AAT 624
 QY 1224 GTAGCGGAGCCCAATATATATATATGATGATTTGAAAAGTATGAGGT 1283

DB 623 ATAAAAAAT 564
 QY 1284 GGGTGGGATTTTAT 1343
 DB 563 TAT 504
 QY 1344 TTGAGTGGGACATCCATAAAGAAAGTATATATATATATATATATATATATAT 1403
 DB 503 TAAAAAT 444
 QY 1404 CCTTAT 1463
 DB 443 AT 384
 QY 1464 ATGAT 1523
 DB 383 ATAAAAAAT 324
 QY 1524 TAT 1583
 DB 323 AT 264
 QY 1584 TTTGTAAAAACAGCTTGGCTCAATGGAAGTTCATGTATTCATATGTTTAAATATA 1643
 DB 263 AATATTTAAAAAAT 204
 QY 1644 AAGTAAATTTTAAAT 1692
 DB 203 AAAAAAT 155

RESULT 4
 CDS0039G 1101 bp DNA 1line GSS 03-JUN-1999
 LOCUS
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL063921.1 GI:4941778
 VERSION
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodes; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr - Web: www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://pacpac.med.buffalo.edu/drosophila_bac.htm.
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 /db_xref="taxon:7227"
 /clone="BACR08K10"

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 DB 548 AA
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 DB 608 NNN
 QY 1095 CTCTTTGAAAAAACAATAGTACTCCCTCCCTCCCTCGAATGTATACATATGATG 1154
 DB 668 AA
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 DB 728 AA
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 DB 788 NAAA
 QY 1275 GTAGTGGGTGGGTGGGATTTTATATATTAATAAATTTACTATTTTGAGAAAGTTTGAAA 1334
 DB 848 AATATATTAAT 907
 QY 1335 TGTATATGAATGTAGTGGAGCATCCATPAAAGGAAAGTATATGAAATTAATGGACAGAG 1394
 DB 908 TATTTNNAAAAATATATNNAAAAATATATATATATATATATATATATATATATAT 967
 QY 1395 GGAGTATACCTTTATGAT 1453
 DB 968 TTTTAT 1027
 QY 1454 CTATGT-TATATATGAT 1510
 DB 1028 TTAAT 1087
 QY 1511 GATTACCGCTTTAT 1570
 DB 1088 AT 1147
 QY 1571 ACCAAATATATCTTGTAT 1630
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 QY 1631 AGTTTAT 1688
 DB 1208 AAT 1267
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 DB 1268 ATTAAT 1327
 QY 1749 AATGATATGCGGTGATCTATGACTTTCACCACTAGTGAATATATGATCTTA 1808
 DB 1328 TAT 1386
 QY 1809 GATATACATCTTTCAATTTCAACAACACAGCTTTTCTTTCACAGGATTTGAA 1868
 DB 1387 AAT 1446
 QY 1869 TCCCTTTCTAAACTTTTAAATATATATATATATATATATATATATATATATATATAT 1928
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 QY 1929 AACATTGATGCTGCTACTATTAAT 1954
 DB 1507 AATTAAT 1532

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 DEFINITION
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 genomic survey sequence.
 ACCESSION
 CG753083
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 CG753083.1 GI:37977199
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 ORGANISM
 Pristionchus pacificus
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 Neodiplogasteridae; Pristionchus.
 REFERENCE
 1 (bases 1 to 1896)
 Bunjfer,J., van der Meulen,M. and Sommer,R.J.
 An integrated physical and genetic map of the nematode Pristionchus
 pacificus
 Mol. Genet. Genomics 269 (5), 715-722 (2003)
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 12884007
 COMMENT
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@uebingen.mpg.de
 Classes: BAC ends.
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 Matches 520; Conservative 0; Mismatches 645; Indels 15; Gaps 4;
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 QY 950 AAGAAATTAATATTAACGAAATCATTTTATATACATGCTCTCGGCTGCTCATTAATATAG 1009

[illegible]

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| Db | | 438 | AA | 497 |
| Oy | | 1228 | CGGAGACCACAATATATTATTGATGATTGAAAAAGTAGTTGAAGTAGTGGTGGCT | 1287 |
| Db | | 498 | AAAAAAAAANNNNNAATATATATTAATTTTTTTTWTATATATTTTTTTTTTTTTTTTT | 557 |
| Oy | | 1288 | GCGATTTTTTATATATATAAAAATTTACATATTTTGGAAGAAGTTGAAATGTATAGATGA | 1347 |
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| Oy | | 1348 | GTGGACATCCATTAAGAAAGTATAGAAATTTAAATGGACAGAGGAGTAATACCTT | 1407 |
| Db | | 618 | AAAAAATTTTAAAMAAWTTTTTTTTTTTWTTAATTAATTAAMAAAAAATAMAATTTWTTA | 677 |
| Oy | | 1408 | TATGATATAT- AAAATTTTTTGTATTTTGATTTCATAAGATTATAATCTATGTTATATG | 1466 |
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| CNS00EVL | | Drosophila melanogaster genome survey sequence T7 end of BAC: | | |
| LOCUS | | BACR2B23 of RFLI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. | | |
| DEFINITION | | AL069706 | | |
| ACCESSION | | AL069706 | | |
| VERSION | | GI:4949849 | | |
| KEYWORDS | | GSS. | | |
| SOURCE | | Drosophila melanogaster (fruit fly) | | |
| ORGANISM | | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydraidea; Drosophilidae; Drosophila. | | |
| REFERENCE | | 1 (bases 1 to 1101) | | |
| AUTHORS | | Genoscope. | | |
| TIITLE | | Direct Submission | | |
| JOURNAL | | Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr | | |
| COMMENT | | - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of | | |

COMMENT

1-7-22 Sueniyo-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
E-mail: hatoric@isc.riken.jp, url: <http://hsp.ise.riken.go.jp/>
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the mouse BAC library M5MG01. For BAC
library availability, please contact Kuniya Abe (abe@crc.riken.jp)
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

Sequencing : T7

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Vector      : pBACe3.6
R.Site 1    : EcORI
R.Site 2    : EcORI.
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| Best Local Similarity | 45.5% | Pred. No | 3 | 99.0% | | | |

Matches 471; Conservative 0; Mismatches 551; Indels 14; Gaps 4

[illegible]

| RESULT 13 | CG757503/c | | | | |
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| LOCUS | CG757503 | | | | |
| DEFINITION | CG757503 | 1392 bp | DNA | linear | GSS 24-OCT-2003 |
| ACCSSION | CG757503 | CG5-4-C08.2a | pPa | EcoRI | BAC Library |
| VERSION | CG757503 | | | | Pristionchus pacificus genomic.c. |
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| SOURCE | GSS. | | | | |
| | Pristionchus pacificus | | | | |

Neodiplogasteridae; Pristionchus.
1 (pages 1 to 1392)

REFERENCE 1 (bases 1 to 1392)

TITLE Buntjer, J., van der Meulen, M. and Sommer, R. J.
An integrated study of the
Schilvassan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Schilvassan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R. J.

JOURNAL
of
Molecular
Evolution
269 (5), 715-722 (2003)

PUBMED 12884007
COMMENT Contact: Sommer BJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371

Fax: 0049 7071 801458
 Email: ralf.sommer@tuebingen.mpg.de
 Class: PAC ends

| FEATURES | Location/Qualifiers |
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ORIGIN

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Best Local Similarity 43.8%; Pred. No. 3.9e-06;
Matches 543; Conservative 0; Mismatches 672; Indels 24; Gaps 3;

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Db 519 ATTATATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 460
QY 1366 GAAAGCTATAGATTAATGAGACAGAGGAGTAATACCTTTATGATATATAATTTT 1425
Db 459 TAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 400
QY 1426 GTTATTTGATTTCAATAGATTATAATCTATGTTTATTAATATATAATTTTAAAT 1485
Db 399 AATATATATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 340
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Db 339 AATATATATAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 280
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QY 1606 AATGGAGAGCTGATGATGATTAATGATTTTATATATATAATTAATTTTAAATTTG 1665
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DEFINITION genomic survey sequence.
ACCESSION CC253231
VERSION CC253231.1 GI:30589981
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SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1277)
AUTHORS Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 18200 Std Error: 0.00
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Clase: BAC ends
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CH261 Female Chicken library - for library and clone
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ORIGIN
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 13:22:10 ; Search time 1181.48 Seconds
(without alignments)
10331.389 Million cell updates/sec

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Perfect score: 2052
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 93 | 4.5 | 3673778 | 16 | US-10-312-841-1 |
| 3 | 91.8 | 4.5 | 8056 | 18 | US-10-473-126-240 |
| 4 | 91.6 | 4.5 | 8056 | 18 | US-10-473-126-386 |
| 5 | 88.6 | 4.3 | 8056 | 18 | US-10-473-126-240 |
| 6 | 83 | 4.0 | 158001 | 17 | US-10-211-179-11 |
| 7 | 79.4 | 3.9 | 74685 | 18 | US-10-719-993-6854 |
| 8 | 75 | 3.7 | 11745 | 15 | US-10-240-453-206 |
| 9 | 71 | 3.5 | 5930 | 15 | US-10-311-455-490 |
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| 11 | 70 | 3.4 | 3252 | 13 | US-10-027-632-113786 |

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| C 13 | 70 | 3.4 | 3252 | 13 | US-10-027-632-113788 | Sequence 113788, |
| C 14 | 70 | 3.4 | 3252 | 13 | US-10-027-632-113786 | Sequence 113786, |
| C 15 | 70 | 3.4 | 3252 | 17 | US-10-027-632-113787 | Sequence 113787, |
| C 16 | 70 | 3.4 | 3252 | 17 | US-10-027-632-113788 | Sequence 113788, |
| C 17 | 69.8 | 3.4 | 6352 | 17 | US-10-221-613-195 | Sequence 195, App |
| C 18 | 69.4 | 3.4 | 16258 | 17 | US-10-257-166-120 | Sequence 120, App |
| C 19 | 69 | 3.4 | 3673778 | 16 | US-10-312-841-2 | Sequence 2, App |
| C 20 | 68.6 | 3.3 | 49979 | 18 | US-10-741-601-5746 | Sequence 5746, A |
| C 21 | 68.6 | 3.3 | 49979 | 15 | US-10-311-455-2128 | Sequence 2128, A |
| C 22 | 68.2 | 3.3 | 15348 | 18 | US-10-311-455-191 | Sequence 191, App |
| C 23 | 68 | 3.3 | 11422 | 17 | US-10-257-166-17 | Sequence 17, App |
| C 24 | 67.8 | 3.3 | 15732 | 15 | US-10-239-676-95 | Sequence 95, App |
| C 25 | 67.8 | 3.3 | 15732 | 14 | US-10-240-453-107 | Sequence 107, App |
| C 26 | 67.8 | 3.3 | 15732 | 15 | US-10-433-793-24 | Sequence 24, App |
| C 27 | 67.6 | 3.3 | 5984 | 18 | US-10-311-455-1984 | Sequence 1984, App |
| C 28 | 67.6 | 3.3 | 6050 | 15 | US-10-311-455-1115 | Sequence 1115, App |
| C 29 | 67.4 | 3.3 | 5748 | 15 | US-10-311-455-228 | Sequence 228, App |
| C 30 | 67.4 | 3.3 | 18154 | 15 | US-10-311-455-1128 | Sequence 1128, App |
| C 31 | 67.2 | 3.3 | 5807 | 15 | US-10-723-860-7676 | Sequence 7676, App |
| C 32 | 67.2 | 3.3 | 6816 | 18 | US-10-027-632-97533 | Sequence 97533, A |
| C 33 | 67 | 3.3 | 2053 | 13 | US-10-027-632-97533 | Sequence 97533, A |
| C 34 | 67 | 3.3 | 2053 | 17 | US-10-027-632-97533 | Sequence 97533, A |
| C 35 | 67 | 3.3 | 115218 | 19 | US-10-278-698-255 | Sequence 255, App |
| C 36 | 67 | 3.3 | 115218 | 19 | US-10-278-698-769 | Sequence 769, App |
| C 37 | 66.6 | 3.2 | 419 | 9 | US-09-960-352-11234 | Sequence 11234, A |
| C 38 | 66.6 | 3.2 | 6079 | 15 | US-10-311-455-1934 | Sequence 1934, App |
| C 39 | 66.6 | 3.2 | 6292 | 17 | US-10-221-744-461 | Sequence 461, App |
| C 40 | 66.4 | 3.2 | 18624 | 15 | US-10-311-455-1676 | Sequence 1676, App |
| C 41 | 66.2 | 3.2 | 1501 | 18 | US-10-473-126-328 | Sequence 328, App |
| C 42 | 66.2 | 3.2 | 3252 | 13 | US-10-027-632-113786 | Sequence 113786, |
| C 43 | 66.2 | 3.2 | 3252 | 13 | US-10-027-632-113787 | Sequence 113787, |
| C 44 | 66.2 | 3.2 | 3252 | 13 | US-10-027-632-113788 | Sequence 113788, |
| C 45 | 66.2 | 3.2 | 3252 | 17 | US-10-027-632-113786 | Sequence 113786, |

ALIGNMENTS

RESULT 1
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 4.8%; Score 99.4; DB 18; Length 8056;
Best local similarity 44.5%; Pred. No. 1.1e-07;
Matches 624; Conservative 0; Mismatches 761; Indels 18; Gaps 5;

| | | | |
|----|------|---|------|
| QY | 548 | ANGCTTCTCAAAAGTTTATATATGTAATATGATCCATCCAGAGTAAGTAATTC | 607 |
| DB | 1975 | ATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT | 2034 |
| QY | 608 | CCGTTTAACCACTTCTTATATATATATATATATATATATATATATATATATATAT | 667 |
| DB | 2035 | ATTTTAAATATTTTATTTTATTTTAAATTTTATTTTAAATTTTATTTTAAATTTTAAAT | 2094 |
| QY | 668 | TTAGACGACAAAGACTTATGTCATTAATGACGCTGTAAACAGCTAGACTGCTCAC | 727 |

[illegible][illegible]


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US-10-719-993-6854
RESULT 7
US-10-719-993-6854
; Sequence 6854 Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6854
; LENGTH: 74665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6854

```

| Matches | Conservative | Mismatches | Indels | Gaps |
|---------|--------------|------------|--------|------|
| 584; | 0; | 691; | 30; | 6; |

Oy 637 TTACACTTAACAAGGATATTCTAATPACTTTTGAACGCAAGACACTTAGTCATAAAAT 696
 Db 54564 TTTGTCCAAAABAAATATATATATATATGGATTTTTTATATATATATATATATATATATG 54622
 Oy 697 GGACCGTGTTAAACAGCCTAGAAGCTTGTCACATGATAAAATAGATAATGTTATATAT 756
 Db 54624 AATGTGAAATATATTTAAATAATATATATATATATATAGTAATATATATATATATATAT 54683
 Oy 757 AGTAGATCACAAATACACTTAAAAATYAGACTATTTAAATYAGTAACTAAATAATAGAG 816
 Db 54684 ATTTATATATNGTRAT 54743
 Oy 817 AGGTAGTAAACGAAGCAGGTAAAAACAAGCTGCCTGCTGCTGTAGTTGTGT 876
 Db 54744 ATTAAAT 54803
 Oy 877 GAGCATATCTCTTAAAAAGVATGTAACGATCTAAAGCACATGAAATTAGTACAG 936
 Db 54804 AAATANGTAT 54863
 Oy 937 TTAAAACTTTCAAAGAAATTTATATATAAACGAATCAATTTATTAACATGCTCTCGGCT 996
 Db 54864 ATTTAT 54923
 Oy 997 GTCATTTATATAGGATCACTTATCGATCAATGCCATTAAAAACCCTGTTAAACAAATTQAA 1056
 Db 54924 TAAATTAAT 54982
 Oy 1057 TGAGTTAAATATATCTTACAATGAAAAGAGACAAATGCTCTTTGAAAAAACAAATAGST 1116
 Db 54983 TAGTGTAATATATTTAT 55042
 Oy 1117 ACTCCCTCCGCTCTGGAATGTATACATATATATATATATATATATATATATATATATATAT 1176
 Db 55043 AATATGTAAT 55089

[illegible]

RESULT 8
US-10-240-453-206/c
Sequence 206, Application US/10740453
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
FILE REFERENCED: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06


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; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 206
; LENGTH: 11745
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (9105)
US-10-240-453-206

Query Match      3.7%; Score 75; DB 15; Length 11745;
Best Local Similarity 42.7%; Pred. No. 0.0027;
Matches 499; Conservative 0; Mismatches 665; Indels 5; Gaps 2;

QY 768 CAATGACATTAATTAAGCTATTATTAAGTTACTAATAATAAGAGAGGTTAGTAAA 827
DB 4805 CGAATTAATTAATTAATTTCTAATTTCTAATAATAATAATAATAATAATAATAATT 4746
QY 828 CAGAAAGCGTAAAAACAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
DB 4745 AATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4686
QY 888 TTTAAAGTATGTAATGATCTAAGACATAGAAATTTAGTACAGGTTAAACCTTT 947
DB 4685 CTCATTCACATCTACCTAATAATAATAATAATAATAATAATAATAATAATAATACTTA 4626
QY 948 ACAAGAATTTATTAATAACGAAAAATCAATTTATTAACATGCTCTCGCTGCTATTAAAT 1007
DB 4625 AAAAAAATAATACTAATAATAACATTTTAAATAATACATCAATAATAATAATAATAATT 4566
QY 1008 AAGGATCACTTATGATCTCTTAAACCTTTGTTAAACCAATTCATGATGATAAAT 1067
DB 4565 ACCTTAAATTTAATCTGAATCTCACTAAA---AAAAAACAATTAATAATAATAATAATA 4509
QY 1068 ATCTTCAATGAAGAAAGAGACAAATGCTCTTTGAAAAAACAATAGTACTCCCTCGT 1127
DB 4508 ACCAAAAACAATAATACTAATCACTTAACATTTAAATACTTAATAATAATAATAATAACA 4449
QY 1128 CCTCTGAATATGATCATATGATGATGACACGAGACTTAAGAAAAATGATTAAGTAAT 1187
DB 4448 AAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4389
QY 1188 GTAGAGTAAAAAGAAAGAAAGAAAGAGGTAAGTAAAGTAAAGGAGCCCAATATATTA 1247
DB 4388 ATTAACATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4331
QY 1248 TTGATGATTTTGAAGAGTATGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1307
DB 4330 TTTAAATCTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4271
QY 1308 ATTTACTATTTTGAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1367
DB 4270 TATTTTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4211
QY 1368 AAGTGTATGAATTAATGAGAGAGAGAGAGTAAATCTTTATGATATTAATTTTGT 1427
DB 4210 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4151
QY 1428 TATTTGATTTTCAAGATTAATAATCTATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1487
DB 4150 TTCTACTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4091
QY 1488 TACTATATTAATTCGATTAAGTACGCTTTTATTAATTTTCAATACTGATTAAT 1547
DB 4090 TTTTCTTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4031
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QY 1548 ATGAATTAATCAGTATCTGAAGAAATATATCTTTGTAATAACAGCGTTCGTCAAA 1607
DB 4030 AAAAAAACAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3971
QY 1608 TGGGAAGTTCATGATGATCAATGATTAATAATAAGTAAATTTAATAATTTGTTA 1667
DB 3970 AAACATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3911
QY 1668 TTTTGTTCAGAAATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1727
DB 3910 AAACCTTCATTTTAACAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3851
QY 1728 GCAGCACTAGCTGTTTGAACATGATGTCGGGTATCATGATCACTTCAATCACTCA 1787
DB 3850 TAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3791
QY 1788 ACTAGTAATAATGCAATTTTGAATAATCAATCTTTCAATTTCAACAAACAGCTTTAAC 1847
DB 3790 AACATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3731
QY 1848 TTTTCTTCAAGATTTGAATCTTTCTTAACCTTTTAAATTAATAATAATAATAATGCAATT 1907
DB 3730 TTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3671
QY 1908 TGTAAATTTATCAACACCTCAACATTTGA 1936
DB 3670 TTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3642

RESULT 9
US-10-311-455-490/C
; Sequence 490, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 490
; LENGTH: 5930
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-490

Query Match      3.5%; Score 71; DB 15; Length 5930;
Best Local Similarity 46.4%; Pred. No. 0.011;
Matches 371; Conservative 0; Mismatches 420; Indels 8; Gaps 4;

QY 897 AATGTAATCTGATCTTAAGACATAGAAATTTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 956
DB 5154 AATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 5095
QY 957 TATTAATAAGAAATCATTTATTAACATGCTCTCGGCTGCTCATTAATATAGAGATCAC 1016
DB 5094 ATTTTAAAAAATTTAGTCATCAAACTTATCTTAATAAACTCAAACTCCCAATTTATAT 5035
QY 1017 TTAGTATCATCATTAATAAACCTTTGTAACAAATTCATAGATTAATAATCTTTACAA 1076
DB 5034 CTAAATTAATAATAATTTCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATA 4975
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[illegible]

RESULT 11
US-10-027-632-113786/c

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Sequence 113786, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 113786
LENGTH: 3252
TYPE: DNA
ORGANISM: Human
OS-10-027-632-113786

```

| | | | | |
|---------------------------|-------|------------------|------------|--------------|
| Query Match | 3.4% | Score 70; | DB 13; | Length 3252; |
| Best Local Similarity | 43.6% | Pred. No. 0.014; | | |
| Matches 474; Conservative | 0; | Mismatches 600; | Indels 14; | Gaps 3; |

[illegible]

Db 2254 TATTTAAGTGTATGGTACATATGATAAGTAAATATATTAATTTAATATATAATAC 2195

741 ATTGTAGTATATAGTAGGATCTCAATGACATTAATAATTAGAGCTATTAACT 800

DB 2194 ATTATATATATAATTTTAAACCAATATATCATATATACATTAATTCATATATATATATTTTAAATA 2135

QY 801 TACTA-----ATTAATTAAGAGAGTTAGTAAACAGAAAGCAAGTAAATAACAG 848

Db

2134 TATTAATACCATATAA TAACTATATATTTAAAAAGCTAATTTATATATTTACATTTAACTACTAATA 2075

DB 2074 ACTTTAACTAATTGTTAACTACATTAATAATTAATAATTAATACTATATTA 2015

QY 909 TCTAAGCACATAGAAATTAGTACAGGTTA-AAACITTTACAGAATTATATATTAACG 967

[illegible]

1028 CCAATTAACCCCTGTTAAAAACAATTCTCATGAGTAAAAATATCTTACCAATGAAAAGAGG 1087
Db 1954 TGAATATATTAATATATATTAATTTGCAATTTTATTTATTAATATTAATTTATTAATTTAAAT 1895

Db 1894 ATAAATATTATATATATATTTAAATCAACATATTATATATATATATATTCATAAAC 1835

OY 1088 ACAATGCTCTTTGAAAAAACAATAGTAGTCCCTCCGTCCTCGAAATGTATTACATA 1149
1834 AATATTATATATATATATATTTATTAACAATATATATATATATATTTATATATACAAATAT 1775

QY 1148 TGGATTGACACGAGACTTAAGAAAAATGTATTAAGTAATGTAGATTAAGAAAAAGAGA 1207

| | | | |
|----|------|---|------|
| Db | 1774 | TATATATTATATATATTTAATATACCAATATTTATATATATATATATATTTAATATACCAATA | 1715 |
| Yv | 1208 | AAGAAAGTGGGTAAAGTAGCCGGACCCACCATATATATTAATTGTAGATTTAGAAAAGTA | 1262 |

Db 1714 TTTATATATTATATATATTAAATACATATTATTATATATTATATATATTTTAAATACAA 16555

Qy 1268 GTTGAAGTACGGGTGGGATTTTATATATATAAAATTACTATTTTGAAAGT 1327

1654 TATTTATATATATATATATTTTATATACATATTTATATATATATATATATAA 1539

1328 TTTGAAATGTATGAATTGAGTGGGACATCCATAAAGGAAGCTATATGAATTAAATGG 1387

| | | | |
|----|------|--|------|
| Dd | 1594 | TTTATAATTATAATTGATTGATCATACATAATTATTATATCAATATATCATTAATA | 1595 |
| Dy | 1388 | GACAGAGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATTTCATAGATT | 1442 |

Db 1534 TTAATATATGAACTACTTAATATATGAAATATATTGCTATTCTTATATATTAATATATAAGA 1475

QY 1448 ATAAATCTATGTATATATGAT- ATATATATTTTAAAAATTAATCTATATTTTAAATCTGAT 1506

Db 1474 ATATATATATATATATGTATTATATATACATATTTATAGATTATATATAATATCATTTGTA 1415

1507 AGTCGATTACCGCCTTTATATTTTACATCTAGTAAATATGATAATCATCTATCT 1566

| | | | |
|----|------|--|-------|
| Qy | 1567 | GAAAGCAATATATCTTTGTGAAACAGCGTTCCGTCAAATGGGACGTCATGCTGTAAT | 16288 |
| Db | 1414 | TATTATGTAATGATTTATATATGTTATATATAATATGAATGCAAAATTATATATAATATA | 13555 |

Db 1354 TTATATATATATATATATATATTCATATATTTATATATTTAAATGTTAACTATA 1295

QY 1627 CATAGCTTTTATATATAAAGGAAATTTTAAATTAATGTTATTTTGGTTCCAGAAATTTA 1686

Db 1294 TATTAATGTTACATATTAATTAAGTTAATTCTATATTAATTAATTAATTAATTAAGTTAA 1235

| | | | |
|----|------|----------|------|
| QY | 1687 | AAATAAAT | 1694 |
| | | | |
| | 1694 | CTCTTCTT | 1697 |

DD 1234 CAGIANGI 1221

RESULT 12

```

US-10-027-632-113787/c
; Sequence 113787, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113787
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113787

Query Match      3.4%; Score 70; DB 13; Length 3252;
Best Local Similarity 43.6%; Pred. No. 0.014;
Matches 474; Conservative 0; Mismatches 600; Indels 14; Gaps 3;

QY 621 TTGTTAATATATATATGTTTACACTTACAGAGATATTCGTAATCTTTAGACAGCAAGA 680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2314 TTAATACCTAACAAATTTTATCTATATATATGAGTTAATATGTTTATACCTGTAATATA 2255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 681 GACTTAAGTCAAAATGAGCGCTGTAAACAGCCTAGACTTGCTCATGTATTAATAGATA 740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2254 TATTTTACTGTATGTAACATATGTAATGTAATATATATATATATATATATATATATAC 2195
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 741 ATTGTTAGTATATATATAGATCTCAATGACATTAATAATAGAGCTATTAATTAAGT 800
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2194 ATTATATATATATATATTAACAAATATATCATTAATCATTAATTAATTAATTAATTA 2135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 801 TACTA-----ATTAATPAGAGAGTTAGTAAACAGAGACAGTAAACAG 848
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2134 TATATATCCATATATATCTTATATTAATAAGCTAATTAATATATATATATATATATAT 2075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 849 AGCTGCTGCTGTGTGTTTGGTTGTGAGCTCATTTCTTTAAAGTATGTAATGTA 908
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2074 ATCTTATATCTTATGTTTAACTTACATTAATAATTAATTAATTAATTAATTAATTA 2015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 909 TCTPAAAGCATGAAATTTAGTACAGGTTA-AACTTTACAGAAATTTATATTAACG 967
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2014 TCTGTTAATCTATATATATATAGTTAACATTAATAAATATATATATATATATATAT 1955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 968 AAAATCAATTTTAAATGCTCTGCGCTGCTATATATATAGGATCTACTGATCAT 1027
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1954 TGTATATATATATATATATATGCAATTTATATATATATATATATATATATATATAT 1895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1028 CCATTTAAACCTTTTAAACAAATTCATGATGATTAATATCTTACATGAAAGAGG 1087
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1894 ATTAATATATATATATATATATATTAATTAACAAATTTATATATATATATATATAT 1835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1088 ACAATGCTCTTTGAAAAAAGAAATAGTACTCCCTCCGCTCCCTGAAATGATATACATA 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1834 AATATTTATATATATATATATATATTAATTAACAAATATATATATATATATATATAT 1775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1148 TGGATTGACACGAGACTAAGAAAAATGTATTAAGTATAGTAAAGAAAAAGAAAGAG 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 1774 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1208 AAGAAAAGTGGGAAAGTACGGGACCCACCAATATATATATGATGATTTGAAAGATA 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1714 TTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1268 GTTGAAGTATGAGGAGGAGGATTTTATATATATATATATATATATATATATATAT 1327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1654 TATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1328 TTTGAAATGATATGAAATGAGTGGACATCCATTAAGAAAGTATAGATTAATGAG 1387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1594 TTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1388 GACAGAGGAGTAAATACCTTATGATATATATATATATATATATATATATATATAT 1447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1534 TTAATATATGAAATATCTATTAATATATATATATATATATATATATATATATATAT 1475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1448 ATTAATCTATGTTATATATATATATATATATATATATATATATATATATATATAT 1506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1474 ATTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1507 AGTCATTTACCGCCCTTTTATATATATTTTACATATGAGTATATGATTAATCACTAT 1566
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Db 1414 TATATATGTAATGATTTATATATATGTTATATATATATATATATATATATATATAT 1355
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QY 1567 GAAAAACAATATATATCTTTGTAACAGCGCTGCTCAATGGAGTCAATGATAT 1626
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Db 1354 TTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 1295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1627 CAATGTTTATATATATATATATATATATATATATATATATATATATATATATAT 1686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1294 TATATATGTAACATATTAATTAAGTTATATATATATATATATATATATATATATAT 1235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1687 AAATTAAT 1694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1234 CAGTAAGT 1227
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RESULT 13
US-10-027-632-113788/c
; Sequence 113788, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113788
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113788

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| | Best Local Similarity | 43.6%; Pred. No. 0.014; Gaps 3; |
| | Matches | 474; Conservative 0; Mismatches 600; Indels 14; |
| Qy | 621 TTGTTAATATATATAGTTTACCTTAACAAGAGATATTGTATATACTTTTAGACGACAGA | 680 |
| Db | 2214 TTAATATCAAAATTTTTATCTTATATTAATGAAGTTAATATGTTTATACGTAAATTA | 2255 |
| Qy | 681 GACTTAGTCMAAAATGACCGCTGGTAAACAGCCTAGACTTGTCATGATPAATAGATA | 740 |
| Db | 2254 TAATTAACGTGTATGTGTAACATATGAAATAGTAATATATTAATTTAAATATATATAC | 2195 |
| Qy | 741 ATTCTTAGTAAATATATAGTAGACTCCACAGACCTTAAATTTAGCATTAATTAAGT | 800 |
| Db | 2194 ATATTAATATATAATTTATATACAAATATATACATATATCATATTTATATATTTAATA | 2135 |
| Qy | 801 TACTA-----ATAATAGAGAGGTATGTAACAGAAAGCAGTAAACAG | 848 |
| Db | 2134 TATATATACAAATATACCTTATATTTAAAAGCTAATTTAATATATACATTAACTATATA | 2075 |
| Qy | 849 AGCTTGCTGCTGTGTGTAGTTGTTGTGAGCTCATTTCTTTAAAGTAATGTAACTGA | 908 |
| Db | 2074 ATCTTTATCTTATATGTTAACCTTACATTAATTAATTAATATATTAATTAATTAATTA | 2015 |
| Qy | 909 TCCTAAGCACATAGAAATTTAGTACAGGTTA-AACTTTACAGAAATTTATATTTAAACG | 967 |
| Db | 2014 TCTGTGTAACTATATATATATATATGTTAACATATTTAAATATATATATATATATCA | 1955 |
| Qy | 968 AAATATCATTTATATACAGTCTCTCGGCTGCATTATATATAGGGATCACTTACATCAT | 1027 |
| Db | 1954 TGATATATATATATATATATATTTGCATTTATTTATTTATATATATATATATTTAAAT | 1895 |
| Qy | 1028 CCATTAAAACTTGTTAAACAAATTCATGAGATAAATATCTTACAATGAAAGAAAG | 1087 |
| Db | 1894 ATAAATTTATATATATATATATATTTAATTAACAAATTTATATATATATATATCAATAAC | 1835 |
| Qy | 1088 ACAATGCTCTTTGAAAAAACAATAGTACTCCCTCCGCTCCCTGAAATGTATCAATA | 1147 |
| Db | 1834 AATTTTATATATATATATATATTTAATTAACAAATATATATATATATATATATATATAT | 1775 |
| Qy | 1148 TGGATTGGACCGGAGACTAGAAAAATATGTAATGTAAGTAAAGAAAGAAAGAA | 1207 |
| Db | 1774 TATATATTTATATATTTTAAATATACAAATTTATATATATATATATATATATATACATA | 1715 |
| Qy | 1208 AAGAAAGATGGGTAAAGTACGCCGACCACCAATATATAAATGATAGATTGAGAAAGTA | 1267 |
| Db | 1714 TTTATATATATATATATATATTTAAATATACAAATTTATATATATATATATATATATACAA | 1655 |
| Qy | 1268 GTTGAAAGTACGGGTGGGTGGGATTTTATATATATAAAAATTTATCTATTTTGAAAGT | 1327 |
| Db | 1654 TATTTATATATATATATATTTAATATACAAATTTTATATATATATATATATATATATATA | 1595 |
| Qy | 1328 TTTGAAATATGTAATATGTAAGTGGGACATCCATATAAAGAAAGGTATAGAAATTAAGG | 1387 |
| Db | 1594 TTTATATATATATATATATATGATTGTATCAACATATATATTTATATCAAAATATATCAATATA | 1535 |
| Qy | 1388 GACAGAGGAGTAATACCTTATATGATATATATAATTTTGTATTTTGAATTCATAGAT | 1447 |
| Db | 1534 TTTATATATGAAATCTATTAATATATGAAATATATTTGCAATTTCTTATATATATATATAGA | 1475 |
| Qy | 1448 ATAAATCTATGTATTAATGATA-ATATATTTTAAAAATTAATCTATATATATCTGAT | 1506 |
| Db | 1474 ATATATATATATATATATGATATATATATATCTATATATATATGATTTAATAATATATCATTTGTA | 1415 |
| Qy | 1507 AGTCGATTAACGCCCTTTTATATAATTTTACAAATGAGAAATATGAAATTAATCAAGTATCT | 1566 |
| Db | 1414 TATATATGTAATTGATTTTATATATGTTATATATATATATGTAATGCAAAATATATATATATA | 1355 |
| Qy | 1567 GAAGAGCAATATATATCTTTGTAACAAAGCCTCGCTCAAAATGGGAATCATATGATAT | 1628 |
| Db | 1354 TTTAT | 1235 |
| Qy | 1627 CAATAGTTTATATATAAAAAGTAATTTTAAATTAATGTTATTTTGTTCAGAAATTTA | 1686 |

| Db | 1294 | TATTAATAGTACGATATTAATTAAGTTAACTTACTATATTAATTAATTAATTAATTAAGTTAA | 1235 |
|--|------|--|------|
| Qy | 1687 | AAATTAAT 1694 | |
| Db | 1234 | CAGTAAGT 1227 | |
| <p>RESULT 14</p> <p>US-10-027-632-113786/c</p> <p>; Sequence 113786, Application US/10027632</p> <p>; Publication No. US20030204075A9</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Wang, David G.</p> <p>TITLE OR INVENTION: Identification and Mapping of Single Nucleotide</p> <p>FILE OF INVENTION: Polymorphisms in the Human Genome</p> <p>FILE REFERENCE: 108827.129</p> <p>CURRENT APPLICATION NUMBER: US/10/027,632</p> <p>PRIOR FILING DATE: 2002-04-30</p> <p>PRIOR APPLICATION NUMBER: US 60/218,006</p> <p>PRIOR FILING DATE: 2000-07-12</p> <p>PRIOR APPLICATION NUMBER: US 60/198,676</p> <p>PRIOR FILING DATE: 2000-04-20</p> <p>PRIOR APPLICATION NUMBER: US 60/193,483</p> <p>PRIOR FILING DATE: 2000-03-29</p> <p>PRIOR APPLICATION NUMBER: US 60/185,218</p> <p>PRIOR FILING DATE: 2000-02-24</p> <p>PRIOR APPLICATION NUMBER: US 60/167,353</p> <p>PRIOR FILING DATE: 1999-11-23</p> <p>PRIOR APPLICATION NUMBER: US 60/156,358</p> <p>PRIOR FILING DATE: 1999-09-28</p> <p>PRIOR APPLICATION NUMBER: US 60/146,002</p> <p>PRIOR FILING DATE: 1999-08-09</p> <p>NUMBER OF SEQ ID NOS: 325720</p> <p>SOFTWARE: FastSeq for Windows Version 4.0</p> <p>SEQ ID NO 113786</p> <p>LENGTH: 3252</p> <p>TYPE: DNA</p> <p>ORGANISM: Human</p> <p>US-10-027-632-113786</p> | | | |
| <p>Query Match 3.4%; Score 70; DB 17; Length 3252;</p> <p>Best Local Similarity 43.6%; Pred. No. 0.014;</p> <p>Matches 474; Conservative 0; Mismatches 600; Indels 14; Gaps 3;</p> | | | |
| Qy | 621 | TTGTTAATATATATATGTTTACCTTACCAAGAGATATTCGTAATCTTTAGACGACACAGA 680 | |
| Db | 2314 | TTAATACTTAACAATTTTATTAATACTTAATTTAATGAGTTAATATGTTTAACTGTAAATATA 2255 | |
| Qy | 681 | GACTTAGGTCAAAATGAGCGCTGGTAAACAGCGCTGACCTGATCACTGATTAATAGATA 740 | |
| Db | 2254 | TATTTAACTGTGATGTTGTAACATATGAAATAAGTTAATATTAATTAATTAATTAATTAATAC 2195 | |
| Qy | 741 | ATTGTTAGTAAATATATAGTAGATCTCAATGACATTTAAATTTAGACTTAATTAATAGT 800 | |
| Db | 2194 | ATTATTAATATTAATTTAATTAACAATAATATCAATTAATTAATTTCAATTAATTAATTAATA 2135 | |
| Qy | 801 | TACTA-----ATTAATAGAGAGTTAGTAAACGAAAGACGATTAACAG 848 | |
| Db | 2134 | TATATACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 2075 | |
| Qy | 849 | AGCTTGCTGCTGTGTGTTAGTTGTGTGAGCTCAATTTCTTAAAGTAATGTAACTGA 908 | |
| Db | 2074 | ATCTTTACTTATATTTGTTAACTTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 2015 | |
| Qy | 909 | TCCTAAGCACAATGAATTTAGTACAGGTTA-AACTTTTACAAGAAATTAATTAATTAACG 967 | |
| Db | 2014 | TCTGTGTAACTATATATATATAGTTAAACCATATTTAAATATATTAATTAATTAATTAATTAACA 1955 | |
| Qy | 968 | AAATATCAATTTAATTAACATGCTCTCGCGCTGTCATTTAATTAAGGATCACTTACGATCAT 1027 | |
| Db | 1954 | TGATATATTAATTAATTAATTAATTTGCAATTTTATATTAATTAATTAATTAATTAATTAATAT 1895 | |

QY 1028 CCATTAAACCTTGTAAACAATTCATGATGATAAATTCCTTACATGAAAGAGG 1087
DB 1894 ATTAATTTATATATATATATATTTTAAATBAACATATTTAAATATATATCAATTAAC 1835
QY 1088 ACAATGCTCTTTGAAAAACAATAGGTACTCCCTCCGCTCCCTCGAAATGATACATA 1147
DB 1834 AATATTTATATATATATATATTTAAACAATATATATATATATATATATATATAT 1775
QY 1148 TGGATTGGACACGAGACTAAGAAATGTATTAAGTATGATGATGATGATGATGATGAT 1207
DB 1774 TAT 1715
QY 1208 AAGAAAGTGGGTAAAGTACCGGACCCCAATATATATATATATATATATATATATAT 1267
DB 1714 TTTAT 1655
QY 1268 GTTGAAGTATGAGGGGGGGGATTTTATATATATATATATATATATATATATATATAT 1327
DB 1654 TATTTAT 1595
QY 1328 TTTGAAATGTATAGAAATGAGTGGACATCCATTAAGAAAGATGATGATGATGATGAT 1387
DB 1594 TTTAT 1535
QY 1388 GACAGAGGAGATATCTTTATGATATATATATATATATATATATATATATATATATAT 1447
DB 1534 TTAAT 1475
QY 1448 ATTAATCTATGTAT 1506
DB 1474 ATTAAT 1415
QY 1507 AGTCATTAACGCTTTTAT 1566
DB 1414 TAT 1355
QY 1567 GAAAGCAATATATATCTTTGTAAACACGCTGGCAATGGAGATCTCATGTATAT 1626
DB 1354 TTAAT 1295
QY 1627 CAATATGTTTAT 1686
DB 1294 TAT 1235
QY 1687 AATATATAT 1694
DB 1234 CAGTAAGT 1227

RESULT 15
US-10-027-632-113787/c
Sequence 113787, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 113787
LENGTH: 3252
TYPE: DNA
ORGANISM: Human
US-10-027-632-113787

Query Match
Best Local Similarity 43.6%; Score 70; DB 17; Length 3252;
Matches 474; Conservative 0; Mismatches 600; Indels 14; Gaps 3;

QY 621 TTGTTAT 680
DB 2314 TTAATATCTACATATTTTAT 2255
QY 681 GACTTGGTCAAAAATGACGCTGGTAAACAGCTGACCTGATGATGATGATGATGATGAT 740
DB 2254 TATTTAACTGTAT 2195
QY 741 ATGTTAT 800
DB 2194 ATTAAT 2135
QY 801 TACTA-----ATTAAT 848
DB 2134 TTAATATCAAT 2075
QY 849 AGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
DB 2074 ATCTTAT 2015
QY 909 TCTAAAGCAAT 967
DB 2014 TCTGTTAT 1955
QY 968 AAAATCATTTTAT 1027
DB 1954 TGAAT 1895
QY 1028 CCATTAAACCTTGTAAACAATTCATGATGATAAATTCCTTACATGAAAGAGG 1087
DB 1894 ATTAATTTATATATATATATATTTTAAATBAACATATTTAAATATATATCAATTAAC 1835
QY 1088 ACAATGCTCTTTGAAAAACAATAGGTACTCCCTCCGCTCCCTCGAAATGATACATA 1147
DB 1834 AATATTTATATATATATATATTTAAACAATATATATATATATATATATATATATAT 1775
QY 1148 TGGATTGGACACGAGACTAAGAAATGTATTAAGTATGATGATGATGATGATGATGAT 1207
DB 1774 TAT 1715
QY 1208 AAGAAAGTGGGTAAAGTACCGGACCCCAATATATATATATATATATATATATATAT 1267
DB 1714 TTTAT 1655
QY 1268 GTTGAAGTATGAGGGGGGGGATTTTATATATATATATATATATATATATATATATAT 1327
DB 1654 TATTTAT 1595
QY 1328 TTTGAAATGTATAGAAATGAGTGGACATCCATTAAGAAAGATGATGATGATGATGAT 1387
DB 1594 TTTAT 1535
QY 1388 GACAGAGGAGATATCTTTATGATATATATATATATATATATATATATATATATATAT 1447
DB 1534 TTAAT 1475
QY 1448 ATTAATCTATGTAT 1506
DB 1474 ATTAAT 1415

QY 1507 AGTCATTACCGCCTTTTATTAATTTTACATACAGTAATGAAATTAATCAGTTATCT 1566
Db 1414 TATTATGTAATGATTTTATTAATGTTATATTAATGATGCAATTAATATATATATA 1355
QY 1567 GAAAGCAATATATCTTTGTAACAGCGTTCGTCAAATGGAGTTCAATGTATTT 1626
Db 1354 TTAT 1295
QY 1627 CAATAGTTTATATATTAAGTAATTTTAATTAATTTGTTATTTGTTTCAGAAATTTA 1686
Db 1294 TATATAGTTAGCAATTAATTAAGTTAATTACTATATTAATTAATTAATTAAGTTAA 1235
QY 1687 AAATAAAT 1694
Db 1234 CAGTAAGT 1227

Search completed: March 15, 2005, 18:25:12
Job time : 1198.48 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 10:33:10 ; Search time 7598.94 Seconds
(without alignments)
11023.765 Million cell updates/sec

Title: US-09-806-197-1

Perfect score: 2052

Sequence: 1 catgctgccccacagcaca.....gcataacatcctaataatc 2052

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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| Db | 781 | ATTGAGCTAATTAATTAAGTACTAAATAAATAAGACGTTAGTAAACAGAAGCAGCTA | 840 |
| OY | 841 | AAAACAAGCGTCGTGCTGTGTGTGGTTTGTTGTTGTGTGAGCTCATTTCTTAAAAAGTATG | 900 |
| Db | 841 | AAAACAAGCGTCGTGCTGTGTGTGTGGTTTGTTGTTGTGTGAGCTCATTTCTTAAAAAGTATG | 900 |
| OY | 901 | TAACTGATCTAAGCACATAGAAATTTTAGTACAGGTTAAAACTTTTACAGAAATTTATA | 960 |
| Db | 901 | TAACTGATCTAAGCACATAGAAATTTTAGTACAGGTTAAAACTTTTACAGAAATTTATA | 960 |
| OY | 961 | TTAAACGAATTCATTTATATACATGCTCCCGGTGCATTAATAATGGGATCACTTAC | 1020 |
| Db | 961 | TTAAACGAATTCATTTATATACATGCTCCCGGTGCATTAATAATGGGATCACTTAC | 1020 |
| OY | 1021 | TGATCATCATTTAAACCCTGTGTAAACCAATTCATGAGATTAATAATCTTACATGAA | 1080 |
| Db | 1021 | TGATCATCATTTAAACCCTGTGTGTAAACCAATTCATGAGATTAATAATCTTACATGAA | 1080 |
| OY | 1081 | AAGAAGCAATATCTCTTTGAAAAAACAAATPAGTATCCCTCCGCTCCCTGAATNGT | 1140 |
| Db | 1081 | AAGAAGCAATATCTCTTTGAAAAAACAAATPAGTATCCCTCCGCTCCCTGAATNGT | 1140 |
| OY | 1141 | ATACATATGATTTGGACACACGAGACTAAGAAAAATGTAAAGTATGTAGATPAANAAG | 1200 |
| Db | 1141 | ATACATATGATTTGGACACACGAGACTAAGAAAAATGTAAAGTATGTAGATPAANAAG | 1200 |
| OY | 1201 | AAAGCAAAAGAAAGTGGGTAAAGTAGCGGGGCCACCAATATATATATGATTAAGTTAG | 1260 |
| Db | 1201 | AAAGCAAAAGAAAGTGGGTAAAGTAGCGGGGCCACCAATATATATATGATTAAGTTAG | 1260 |
| OY | 1261 | AAAAGTATGTTGAAGATAGCGGGGTGGAGATTTTATATATATATAAATTTACTATTG | 1320 |
| Db | 1261 | AAAAGTATGTTGAAGATAGCGGGGTGGAGATTTTATATATATATAAATTTACTATTG | 1320 |
| OY | 1321 | AGAAAGTTTTGAATGTATAGAAATTTAGTGGGACATCATAAAGAAAGTGTATAGAT | 1380 |
| Db | 1321 | AGAAAGTTTTGAATGTATAGAAATTTAGTGGGACATCATAAAGAAAGTGTATAGAT | 1380 |
| OY | 1381 | TAAATGGGACAGAGGAGTAAATCCTTTATGATATATATAATTTTGTATTTGATTTTCA | 1440 |
| Db | 1381 | TAAATGGGACAGAGGAGTAAATCCTTTATGATATATATAATTTTGTATTTGATTTTCA | 1440 |
| OY | 1441 | TAAATTTTAAATCTATGTATTAATGATATATATAATTTTAAATAATATATCTATATTAAT | 1500 |
| Db | 1441 | TAAATTTTAAATCTATGTATTAATGATATATATAATTTTAAATAATATATCTATATTAAT | 1500 |
| OY | 1501 | CTGATTAAGTCGATTACCGCTTTTATTAATTTTACAATCTGAGTATATGAAATTAATCAG | 1560 |
| Db | 1501 | CTGATTAAGTCGATTACCGCTTTTATTAATTTTACAATCTGAGTATATGAAATTAATCAG | 1560 |
| OY | 1561 | TTATCTGAAAAGCAAATATATATCTTTGTPAAAAACAGCGTTCCGATCAATGGGAAGTCAAT | 1620 |
| Db | 1561 | TTATCTGAAAAGCAAATATATATCTTTGTPAAAAACAGCGTTCCGATCAATGGGAAGTCAAT | 1620 |
| OY | 1621 | TGATATCAATAGTTTAAATATPAAPAAAAGTAAATTTTAAATTAATGTATTTTGTTCAGA | 1680 |
| Db | 1621 | TGATATCAATAGTTTAAATATPAAPAAAAGTAAATTTTAAATTAATGTATTTTGTTCAGA | 1680 |
| OY | 1681 | AATTTAAATAATATATATGAGATGGGAAGTACCGGGCATCATTGAGACACATAGACT | 1740 |
| Db | 1681 | AATTTAAATAATATATATGAGATGGGAAGTACCGGGCATCATTGAGACACATAGACT | 1740 |
| OY | 1741 | GTTTGAAACATATGATGTCGGGTGTACATCTATGACCTTTCAACTMAACTATGATATAT | 1800 |
| Db | 1741 | GTTTGAAACATATGATGTCGGGTGTACATCTATGACCTTTCAACTMAACTATGATATAT | 1800 |
| OY | 1801 | GCATTTCTGAATATCATCTTTTCAATTTTCAACAAACAGGTTTAACTTTCTTCAACG | 1860 |
| Db | 1801 | GCATTTCTGAATATCATCTTTTCAATTTTCAACAAACAGGTTTAACTTTCTTCAACG | 1860 |

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Oy      1861 GATTGGAATCCTTTCTTCAACTTTTAAATATAAAAAAGCATTAATGTAATTTATC 1920
Db      1861 GATTGGAATCCTTTCTTCAACTTTTAAATATAAAAAAGCATTAATGTAATTTATC 1920
Oy      1921 AACACCTCAACATGATGTAGCGTACTATATAAATAGGTCCTTGAGCTCTACTATCAT 1980
Db      1921 AACACCTCAACATGATGTAGCGTACTATATAAATAGGTCCTTGAGCTCTACTATCAT 1980
Oy      1981 CACATCAATCTTACACCAACAAACCTTGAGCTTAATTTTCTACTTAATTTTCAGCAATAC 2040
Db      1981 CACATCAATCTTACACCAACAAACCTTGAGCTTAATTTTCTACTTAATTTTCAGCAATAC 2040
Oy      2041 ATTCTAAATATC 2052
Db      2041 ATTCTAAATATC 2052

RESULT 2
US-09-806-197-7
; Sequence 7, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NISHIKAWA, SATOMI
; APPLICANT: OEDA, KENJI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-7

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| Query Match | 99.8% | Score 2048.8 | DB 35 | Length 2052 |
| Best Local Similarity | 99.9% | Pred. No. 0 | | |
| Matches 2050 | Conservative | 0 | Mismatches 2 | Indels 0 |
| | | | | Gaps 0 |

| | | | |
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| OY | 1 | TATGTGTGCCCTAAGACAATAGGGCCGTGTGGTGAAGAAACAGAGCTGCTTGA | 60 |
| Db | 1 | CATGTGTGCCCTAAGACAATAGGGCCGTGTGGTGAAGAAACAGAGCTGCTTGA | 60 |
| OY | 61 | CTTCCTTCCTTTTGACCTGTGTGTATTAAGAAATAGAAATATTTTTAAAAAGCTGGAA | 120 |
| Db | 61 | CTTCCTTCCTTTTGACCTGTGTGTATTAAGAAATAGAAATATTTTTAAAAAGCTGGAA | 120 |
| OY | 121 | TACTTAACCTTCCTGTCACAACTTCGCGCTCTTTTCCAAACCTTTAATTACTTTTTTACT | 180 |
| Db | 121 | TACTTAACCTTCCTGTCACAACTTCGCGCTCTTTTCCAAACCTTTAATTACTTTTTTACT | 180 |
| OY | 181 | TCTCATTTTCACTCCACCTCTTCCTGCTPAAGCAAGAAATCACTCTTTAAGCTAACCA | 240 |
| Db | 181 | TCTCATTTTCACTCCACCTCTTCCTGCTPAAGCAAGAAATCACTCTTTAAGCTAACCA | 240 |
| OY | 241 | AAGCGCCTCATATAAAGATCATTCATTAATGTATCTTTCATTTTAGGATTAACATACGT | 300 |
| Db | 241 | AAGCGCCTCATATAAAGATCATTCATTAATGTATCTTTCATTTTAGGATTAACATACGT | 300 |
| OY | 301 | GAAACAGGGTTATTTTTTAAACGTGCAACAAATCTTAATATTTTAACTGCGCGGTGAACA | 360 |
| Db | 301 | GAAACAGGGTTATTTTTTAAACGTGCAACAAATCTTAATATTTTAACTGCGCGGTGAACA | 360 |
| OY | 361 | CCGCTCTTCCAAAGATTAATTAATTTTGTAGACCTCCCTTTAACCAATTTGGCAGTC | 420 |
| Db | 361 | CCGCTCTTCCAAAGATTAATTAATTTTGTAGACCTCCCTTTAACCAATTTGGCAGTC | 420 |
| OY | 421 | AGGACGACTTAGTGATATACATTTGATCTGTGAGCTTTTAAACAAAGAACAGTGCTTC | 480 |
| Db | 421 | AGGACGACTTAGTGATATACATTTGATCTGTGAGCTTTTAAACAAAGAACAGTGCTTC | 480 |
| OY | 481 | ATGCTCAGCCATCAAAATTTGACAAACCCGACACAACTGTATCCAGTATCTTACTTT | 540 |

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Db      481 ATGCTCAGCCATCAAAATGACAAAACCGACACAACTCTATCCAGCTACTATACCTT 540
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Db      541 TGGCCCAATGCTCTCAAAATGTTTTTATATGTAATAATATGATCCATCCAGATAAGT 600
Qy      601 AAAATTCGGTTTAAACGAGTTGTTATATATATGTTTACCTTCAAGAGATTTTGT 660
Db      601 AAAATTCGGTTTAAACGAGTTGTTATATATATGTTTACCTTCAAGAGATTTTGT 660
Qy      661 AATATCTTTTAAAGACAGAGAGACTTAAAGTCAAAATGACGCTGGTAAACAGCTAGACT 720
Db      661 AATATCTTTTAAAGACAGAGAGACTTAAAGTCAAAATGACGCTGGTAAACAGCTAGACT 720
Qy      721 TGGTCACTGATTAATATAGATTAATGTTATATATATATATATATATATATATATAT 780
Db      721 TGGTCACTGATTAATATAGATTAATGTTATATATATATATATATATATATATATAT 780
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Db      781 AATTAAGCTATTAATTAAGTTAATAATTAATTAAGAGGTTAGTAAACAGAAACAGGTA 840
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Db      841 AAAACAAGAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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Db      901 TAAACTGATCTTAAAGCAGATAGAAATTTAGTACAGGTTAAACCTTTTCAAGAAATTTA 960
Qy      961 TTAACGAAATTCATTTTATTAACATGCTCTCGGCTGTCAATTAATTAAGGATCACTTAC 1020
Db      961 TTAACGAAATTCATTTTATTAACATGCTCTCGGCTGTCAATTAATTAAGGATCACTTAC 1020
Qy      1021 TGATCATTCATTAACCTTGTAAACAAATTCATTAAGATTAATTAATTCATTAAGTAA 1080
Db      1021 TGATCATTCATTAACCTTGTAAACAAATTCATTAAGATTAATTAATTCATTAAGTAA 1080
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Db      1081 AAGAAGACAAATGCTCTTTTGAAGAAACAAATAGTACTCCCTCGCTCTGAAATGT 1140
Qy      1141 ATACATATGATGACACGAGACTTAAGAAATATTAAGTATATATATATATATATATAT 1200
Db      1141 ATACATATGATGACACGAGACTTAAGAAATATTAAGTATATATATATATATATATAT 1200
Qy      1201 AAAGAGAAAGAAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1260
Db      1201 AAAGAGAAAGAAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1260
Qy      1261 AAAAGTATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
Db      1261 AAAAGTATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
Qy      1321 AGAAAGTTTGAATGATAGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1380
Db      1321 AGAAAGTTTGAATGATAGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1380
Qy      1381 TAAATGAGGACAGAGGAGTAAATACCTTATGATTAATTAATTAATTAATTAATTAAT 1440
Db      1381 TAAATGAGGACAGAGGAGTAAATACCTTATGATTAATTAATTAATTAATTAATTAAT 1440
Qy      1441 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Db      1441 TAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Qy      1501 CTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db      1501 CTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Qy      1561 TTAATCTGAAAGCAATATATCTTTTAAAGCAAGCTTGTGATTAATTAATTAATTAAT 1620
Db      1561 TTAATCTGAAAGCAATATATCTTTTAAAGCAAGCTTGTGATTAATTAATTAATTAAT 1620

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Qy      1621 TGTATTCATATATATATATATATATATATATATATATATATATATATATATATATAT 1680
Db      1621 TGTATTCATATATATATATATATATATATATATATATATATATATATATATATATAT 1680
Qy      1681 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Db      1681 AATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Qy      1741 GTTTGAACATATATATATATATATATATATATATATATATATATATATATATATATAT 1800
Db      1741 GTTTGAACATATATATATATATATATATATATATATATATATATATATATATATATAT 1800
Qy      1801 GCATTCATATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
Db      1801 GCATTCATATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
Qy      1861 GATTTGAATCTTTTCTTAACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
Db      1861 GATTTGAATCTTTTCTTAACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
Qy      1921 AACACCTCAATGATGTTAGCTATATATATATATATATATATATATATATATATATATAT 1980
Db      1921 AACACCTCAATGATGTTAGCTATATATATATATATATATATATATATATATATATATAT 1980
Qy      1981 CACATCAATCTTACACCAAAACCTTGAAGCTTAAATTTTCTACTTATATCTCAGCAATAC 2040
Db      1981 CACATCAATCTTACACCAAAACCTTGAAGCTTAAATTTTCTACTTATATCTCAGCAATAC 2040
Qy      2041 ATTCTAAATATC 2052
Db      2041 ATTCTAAATATC 2052

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RESULT 3
US-09-806-197-5
; Sequence 5, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NISHIKAWA, SATOMI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2056
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-5

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Query Match      99.2%; Score 2034.8; DB 35; Length 2056;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2050; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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Db      1  CANGTGTGCTTACACACATAGAGGCTGTTGTTGAGAGAGAGAGAGAGAGGCTTGA 60
Qy      61  CTCTCTCTCTTTTGAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
Db      61  CTCTCTCTCTTTTGAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
Qy      121  TACTAATCTCTCTGACAACTTCCGCTTTTCCAAACCTTTATTAATCTTTTAACT 180
Db      121  TACTAATCTCTCTGACAACTTCCGCTTTTCCAAACCTTTATTAATCTTTTAACT 180
Qy      181  TCTCATTTCTACTCACTTCTTGTCTATAGCAAGAAATCACTTTTAAAGTAAACCA 240
Db      181  TCTCATTTCTACTCACTTCTTGTCTATAGCAAGAAATCACTTTTAAAGTAAACCA 240
Qy      241  AACGGCTCAATTAAGATCATTCATTAATATATCTTTCAATTTTAAAGTAAACATACGT 300

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Db 241 AACGGCTCAATTAAGATCATTCATTAATGATCTTTCAATTTTGAATTAACAATACGT 300
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Db 301 GAACAGGGTTATTTTAAAGTGTCAACAATCTTAATATTTTACCCTGGCGGTAAACA 360
Qy 361 CGGTCTTCAAGTAATATTTTAAATTTTGTAGCCCTTTTAAACAATTCGATGC 420
Db 361 CGGTCTTCAAGTAATATTTTAAATTTTGTAGCCCTTTTAAACAATTCGATGC 420
Qy 421 AGACAGCTTAGGTGAATACATTTGTAGCTCTTTAAACAAGAACAGTGTTC 480
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Qy 481 ATGCTACGCCATCAAAATTTGACAAAACCGACACAACTCTATCCAGTACTATCTT 540
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Db 601 AAAATTCGGTTTAAACAGTTTGTATATATATGTTTACACTTACAGAGATTTGCT 660
Qy 661 AATACTTTTGAAGCAGACAGACTTAGTCAAAATTTGACAGCTGTGTTAAACAGCTT 720
Db 661 AATACTTTTGAAGCAGACAGACTTAGTCAAAATTTGACAGCTGTGTTAAACAGCTT 720
Qy 721 TGGTCACTGAATATGATTAATTTGATTAATATATAGATCTTAAGATGATTAATA 780
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Db 901 TAAACGATCTAAGACATTAAGAAATTTAGTACAGTTAAACTTTTAAACAAGATTATA 960
Qy 961 TTAACGAAATCAATTTTAAACATGTCTCGGCTGTCAATTAATAGGATCACTTAC 1020
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Qy 1021 TGAATCATCAATTAACCTTTGTTAAACAATTCATGAGATTAATTTTCAATGAA 1080
Db 1021 TGAATCATCAATTAACCTTTGTTAAACAATTCATGAGATTAATTTTCAATGAA 1080
Qy 1081 AAGAAAGCAATGTCTTTTGAAGAAACAATTTGATCTCCCTCCCTCGAATGT 1140
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Qy 1141 ATACATATGATTTGACACGAGACTTAAGAAATTTATTAAGTATGTAAGTAAAG 1200
Db 1141 ATACATATGATTTGACACGAGACTTAAGAAATTTATTAAGTATGTAAGTAAAG 1200
Qy 1201 AAAGAGAAAGAAAGTGGTAAAGTAAAGCGGACCAACAATATATATGATTAAG 1260
Db 1201 AAAGAGAAAGAAAGTGGTAAAGTAAAGCGGACCAACAATATATATGATTAAG 1260
Qy 1261 AAAAGATTTGAAGATGAGTGGTGGGATTTTATTAATTAAGAAATTTACTATTGG 1320
Db 1261 AAAAGATTTGAAGATGAGTGGTGGGATTTTATTAATTAAGAAATTTACTATTGG 1320
Qy 1321 AGAAAGTTTGAATATGATTAAGTGGGATCACTTAAAGGAAAGTATGAAT 1380

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Db 1321 AGAAAGTTTGAATATGATTAAGTGGGATCACTTAAAGGAAAGTATGAAT 1380
Qy 1381 TAAATGGGACAGAGGGAGTAATACCTTATGATATATTAATTTTGTATTTGATTTCA 1440
Db 1381 TAAATGGGACAGAGGGAGTAATACCTTATGATATATTAATTTTGTATTTGATTTCA 1440
Qy 1441 TAAATTTAAATCTATGTTAATATGATTAATTAATTTTAAATTAATCTATATTAAT 1500
Db 1441 TAAATTTAAATCTATGTTAATATGATTAATTAATTTTAAATTAATCTATATTAAT 1500
Qy 1501 CTGATTAAGTCAATACCGCTTTTATATTTTAAACAATCTGAGTAATGAAATTAAG 1560
Db 1501 CTGATTAAGTCAATACCGCTTTTATATTTTAAACAATCTGAGTAATGAAATTAAG 1560
Qy 1561 TTAATCGAAAGCAATATATCTTTGTAACAAGGCTCGGCAATGGGAAGTTCATG 1620
Db 1561 TTAATCGAAAGCAATATATCTTTGTAACAAGGCTCGGCAATGGGAAGTTCATG 1620
Qy 1621 TGAATTCATATGTTTAAATTAATTAATTAATTAATTTTGTTCAGA 1680
Db 1621 TGAATTCATATGTTTAAATTAATTAATTAATTTTAAATTTTGTTCAGA 1680
Qy 1681 AATTTAAATTAATTAATTAAGATGGAAGTTCAAGGATCAATGAGACATTAAGT 1740
Db 1681 AATTTAAATTAATTAATTAAGATGGAAGTTCAAGGATCAATGAGACATTAAGT 1740
Qy 1741 GTTTGAACAATGATGTCGGGTGATCATCTATGACCTTCAACTCAATGATTAAT 1800
Db 1741 GTTTGAACAATGATGTCGGGTGATCATCTATGACCTTCAACTCAATGATTAAT 1800
Qy 1801 GCAATTCAGTGAATGCTTTTCTAATCTTTTAAATTAATTAATTAATTTTCTTTC 1860
Db 1801 GCAATTCAGTGAATGCTTTTCTAATCTTTTAAATTAATTAATTAATTTTCTTTC 1860
Qy 1857 AACGATTTGAATTCCTTTTCTAATCTTTTAAATTAATTAATTAATTTTCTTTC 1916
Db 1857 AACGATTTGAATTCCTTTTCTAATCTTTTAAATTAATTAATTAATTTTCTTTC 1916
Qy 1917 TATCAACACCTCAACATGATGTTAGGCTATTAATTAATTAATTTTCTTTC 1976
Db 1917 TATCAACACCTCAACATGATGTTAGGCTATTAATTAATTAATTTTCTTTC 1976
Qy 1977 TATCAATCAATCTTACACCAAACTTGAAGTAAATTTTCTAATTTCTACAGAA 2036
Db 1977 TATCAATCAATCTTACACCAAACTTGAAGTAAATTTTCTAATTTCTACAGAA 2036
Qy 2037 TAAATTTCTAATATC 2052
Db 2037 TAAATTTCTAATATC 2052
Qy 2041 TCACATTTAAAGATC 2056
Db 2041 TCACATTTAAAGATC 2056

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RESULT 4
US-09-806-197-3
; Sequence 3, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NISHIKAWA, SATOMI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-3

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Query Match 99.0%; Score 2030.8; DB 35; Length 2048;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2046; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

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QY 1 CATGTCGCTACAGACATAGGGCTGTTGGTGAAGAGAGAGAGCTGTTCTGA 60
DB 1 CATGTCGCTACAGACATAGGGCTGTTGGTGAAGAGAGAGAGCTGTTCTGA 60
QY 61 CTTCTCTCTCTTGAAGCTGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 CTTCTCTCTCTTGAAGCTGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 TACTACTCTCTCTCAAGAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 180
DB 121 TACTACTCTCTCTCAAGAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 180
QY 181 TCTCATTTCTACTCCACTCTTCTGCTATAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 TCTCATTTCTACTCCACTCTTCTGCTATAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 AACGGCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 AACGGCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GAACAGAGTTATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GAACAGAGTTATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CCGTCTCTCAAG 420
DB 361 CCGTCTCTCAAG 420
QY 421 AGAGAGAGTTAG 480
DB 421 AGAGAGAGTTAG 480
QY 481 ATGCTCAGCATCAAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATGCTCAGCATCAAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TGGCGGAGAGCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 TGGCGGAGAGCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 AAAATTCCTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 AAAATTCCTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 AAATCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 AAATCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 TGGTCACTGTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 TGGTCACTGTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 ATTAGAGCTATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 ATTAGAGCTATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 AAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 AAAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 TAAAGCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TAAAGCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TTAAGCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TTAAGCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 TGAATCATCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 TGAATCATCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 AAGAAGAGCAATGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 AAGAAGAGCAATGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

DB 1077 AAGAAGAGCAATGCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
QY 1141 ATACATATGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1137 ATACATATGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1196
QY 1201 AAGAAG 1260
DB 1197 AAGAAG 1256
QY 1261 AAAAGTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1257 AAAAGTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1316
QY 1321 AAGAAGTTTGAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1317 AAGAAGTTTGAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1376
QY 1381 TAAATGGAG 1440
DB 1377 TAAATGGAG 1436
QY 1441 TAAAGTTTAAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1437 TAAAGTTTAAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1496
QY 1501 CTGATTAAG 1560
DB 1497 CTGATTAAG 1556
QY 1561 TTATCTGAG 1620
DB 1557 TTATCTGAG 1616
QY 1621 TGAATTCATGATTTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1617 TGAATTCATGATTTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676
QY 1681 AATTTAAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1677 AATTTAAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736
QY 1741 GTTTGAAG 1800
DB 1737 GTTTGAAG 1796
QY 1801 GCATTCATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1797 GCATTCATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
QY 1861 GATTTGAAG 1920
DB 1857 GATTTGAAG 1916
QY 1921 AACACCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1917 AACACCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976
QY 1981 CACATCATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 1977 CACATCATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036
QY 2041 ATTCTAAATATC 2052
DB 2037 ATTCTAAATATC 2048

RESULT 5
US-09-806-197-4
; Sequence 4, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NISHIRAWA, SATOMI

Db 1917 AACCCCAACATTGAGTTCAGCTACTATTAATAGAGTGTCTTGAGTCTACTATCAT 1976
Qy 1981 CACATCAATCTTACACCAACCTTGAGCTTAATTTTCTACTTATTTCTGACATAAC 2040
Db 1977 CACATCAATCTTACACCAACCTTGAGCTTAATTTTCTACTTATTTCTGACATCAC 2036
Qy 2041 ATTCTAAATATC 2052
Db 2037 ATTCTAAATATC 2048

RESULT 6
US-09-300-487-2

/ Sequence 2, Application US/09300487
/ GENERAL INFORMATION:
/ APPLICANT: TORIKAI, Satomi
/ APPLICANT: OEDA, Kenji
/ TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
/ STREET: P.O. BOX 747
/ CITY: FALLS CHURCH
/ STATE: VIRGINIA
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 22040
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/300,487
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,434
/ FILING DATE: 12-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Raymond C.
/ REGISTRATION NUMBER: 21,066
/ REFERENCE/DOCKET NUMBER: 2185-0199P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)205-8000
/ TELEFAX: (703)205-8050
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2042 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Daucus carota L.
/ INDIVIDUAL ISOLATE: Kuroda Gosun
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: 1..2042
/ US-09-300-487-2

Query Match 11.8%; Score 241.2; DB 20; Length 2042;
Best Local Similarity 72.8%; Pred. No. 76-31;
Matches 367; Conservative 0; Mismatches 128; Indels 9; Gaps 4;

Qy 1554 AATCACTATCTGAAAAGCAATATATCTTTGTAAAACAGCG---TTGGTCAATG 1609
Db 1543 AATATATTTATCTGATGATATACATCTTTGTAAAACAACTGGGCAATAGACCAATA 1602
Qy 1610 GGAAGTTCATGTGTATTCATATGTTTATATATAAAGTAATTTTAAATTAATTTTATT 1669
Db 1603 CCAAGTTACGATGATTTTAAATTTTAAATTTTAACTAAACATGATTTTCTT--TTCAAGGT 1660

Qy 1670 TTTGTTCAAGAAATTTAAATTAATTTAGAGTCGGAGTTCAAGGCAATCATTTGAC 1729
Db 1661 ATTAAGTAATTTCTCAATCAATTAATTAATTTGAGCATTTATGAGCACTTATATGCC 1720
Qy 1730 AGCACTAGACTGTTTGAACAATGATGTCGGGTGATACATCTTGAACCTTTGAACGAA 1789
Db 1721 CAGGTGATTTGTTTAAACAACCTTTGTCGGTGTATTTATTTAGACCTTTCAACTAAGC 1780
Qy 1790 TAGTGAAAT-AATGCATTTGAAATATACATCTTTTCAATTTCAACAACAACAGCTTAAT 1848
Db 1781 TAGCCAGTAAATGCTTTCTAGAATATATCTTTGAAATTTCAACAACAACAGCACTAAT 1840
Qy 1849 TTTCTTCAAGCAATTTGAATCCTTTTGAACCTTTTAAATTAATAAATATGACTTAT 1908
Db 1841 TTTCTTCAAGCAATTTGAATGATGCTTTCTTAACTTTTAAAT--AAAAATAACTTACT 1898
Qy 1909 GTTATTTTATCAACCTCAACATTTGATGTTAGCTACTATAATAGTCTCTTGCTG 1968
Db 1899 ATAAATTTTATCAACCTCAACATTTGATGTTAGCTACTATAATAGTCTCTTGCTG 1958
Qy 1969 CTCTACTATCATCATGATCTTACACCAACCTTGACCTTAATTTTCTACTTAT 2028
Db 1959 CTCTACTATCATCATGATCTTCTCAAGCAAACTTGACCTTAATTTTCTACTTAT 2018
Qy 2029 CTCAGCAATTAACATTTCTAAATATC 2052
Db 2019 TTTAGCAAAAACATTTCTAAAGTC 2042

RESULT 7

US-09-300-487-1
/ Sequence 1, Application US/09300487
/ GENERAL INFORMATION:
/ APPLICANT: TORIKAI, Satomi
/ APPLICANT: OEDA, Kenji
/ TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
/ STREET: P.O. BOX 747
/ CITY: FALLS CHURCH
/ STATE: VIRGINIA
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 22040
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/300,487
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,434
/ FILING DATE: 12-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Raymond C.
/ REGISTRATION NUMBER: 21,066
/ REFERENCE/DOCKET NUMBER: 2185-0199P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)205-8000
/ TELEFAX: (703)205-8050
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 247 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:

ORGANISM: Dacus carota L.
INDIVIDUAL ISOLATE: Kuroda Goshun
FEATURE:
NAME/KEY: promoter
LOCATION: 1..247
US-09-300-487-1

Query Match 9.6%; Score 196.6; DB 20; Length 247;
Best Local Similarity 89.6%; Pred. No. 1.8e-23;
Matches 223; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 1804 TTCTAGAAATACATCTTTTCAAAATTCACACACAGCTTAACTTTCTTTCACGAGT 1863
DB 1 TTCTAGAAATATATCTTTTGAAATTCACACACACAGCTTAACTTTCTTTCACGAGT 60
QY 1864 TGAATCCCTTTTCTTAACTTTTAAATTAATAAATGCTTTTGTATATTTATCAAC 1923
DB 61 TAGAATCGTTCTTAACTTTTAAATTT--AAAAATACATTAATAATATTTATCAAC 118
QY 1924 ACCTCAACATTTGATGTAGGCTACTTAATAGTGTCTGTGGCTCTACTATCATCAC 1983
DB 119 ACCTCAACATTTGATGTAGGCTACTTAATAGTGTCTGTGGCTCTACTATCATCAC 178
QY 1984 ATCAATCTTACACACACAACTTGAAGCTTAATTTTCTACTTATTCACGAATTAATT 2043
DB 179 ATCAATCTTACACACAACTTGAAGCTTAATTTTCTACTTATTTTACGAATTAATT 238
QY 2044 CTAAATATTC 2052
DB 239 CTAAAGTTC 247

RESULT 8

US-10-473-126-386
; Sequence 386, Application US/10473126
; GENERAL INFORMATION:
; APPLICANT: Biogenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE: proliferative disorders
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 4.8%; Score 99.4; DB 55; Length 8056;
Best Local Similarity 44.5%; Pred. No. 1.2e-06;
Matches 624; Conservative 0; Mismatches 761; Indels 18; Gaps 5;

QY 548 AAGCTTCGAAATGTTTTTATATGTAATAATATGCCATCCAGATTAAGTAATTC 607
DB 1975 ATTAAATTAATTTTATTTTAAATTAATAATTTTAAATTAATTTTAAATTAAT 2034
QY 608 CCGTTTAAACAGTTTGTATATATATGTTTACACTTACAGAGATTAATTCGTAATCTT 667
DB 2035 ATTTTAAATATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2094
QY 668 TTAGACGACAGAGACTTGTGCTCAAAATGAGCGCTGTAAACAGCTTGTGTAC 727
DB 2095 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2154
QY 728 TGATTAATAGATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 787
DB 2155 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2214
QY 788 CTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 847

DB 2215 AAAAAAAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2274
QY 848 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901
DB 2275 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2334
QY 902 AAATGATCTAAAGACATAGAAATTTAGTACAGTTAAACCTTTTACAGAAATTAAT 961
DB 2335 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2394
QY 962 TAAAGCAAAATCATTTTAAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021
DB 2395 TATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2451
QY 1022 GATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1081
DB 2452 TATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2511
QY 1082 AGAAGACAAATGCTCTTTGAAAAAACAATAGTACTCCCTCCCTGTAATGTA 1141
DB 2512 AATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2571
QY 1142 TACATATGATTTGACACGAGACTTAAGAAAAATGTAATTAATTAATTAATTAAT 1201
DB 2572 TTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2631
QY 1202 AAGAGAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
DB 2632 AAAAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2691
QY 1262 AAATGATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1321
DB 2692 TAAATTTATTTTATTTTATTTTAAATTAATTTTAAATTTTAAATTTTAAAT 2747
QY 1322 GAAAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1381
DB 2748 AAAAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2807
QY 1382 AAATGACAGAGAGGATTAATTAATTAATTAATTAATTAATTTTAAATTTTAA 1441
DB 2808 AAATGTTTATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAAT 2865
QY 1442 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1501
DB 2866 TTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2925
QY 1502 TGAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2985
DB 2926 AATTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 3045
QY 1562 TATCTGAAAAAGCAATTAATTTCTTTTAAACAGCGTTCGCTCAATTTGGGAAT 1621
DB 2986 TTGAAAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 3045
QY 1622 GATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1681
DB 3046 TAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 3105
QY 1682 ATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1741
DB 3106 AATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3165
QY 1742 ---TTTGAACATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1798
DB 3166 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3225
QY 1799 ATGATTTAGATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1858
DB 3226 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3285
QY 1859 CGGATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1918
DB 3286 AATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3345

| | | | |
|----|------|------------------------|------|
| Qy | 1919 | TCAACACTCAACATTGATGTTA | 1941 |
| | | | |
| Db | 3346 | AAATGAATAAATTGGAATGA | 3368 |

RESULT 9

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US-10-266-090-13474
? Sequence 13474, Application US/10266090
? GENERAL INFORMATION:
? APPLICANT: GOLF, STEPHEN
? APPLICANT: BONAN, CAROLINE
? APPLICANT: COLBERT, MICHELLE
? APPLICANT: WANG, RONG-LIN
? TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
? TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
? FILE REFERENCE: NA011,058C1
? CURRENT APPLICATION NUMBER: US/10/266,090
? PRIOR FILING DATE: 2002-10-03
? PRIOR APPLICATION NUMBER: US 10/260,703
? PRIOR FILING DATE: 2002-09-26
? PRIOR APPLICATION NUMBER: US 60/326,117
? NUMBER OF SEQ ID NOS: 51812
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13474
? LENGTH: 1069
? TYPE: DNA
? ORGANISM: HORDEUM VULGARE
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)...(1069)
? OTHER INFORMATION: n = A,T,C or G
US-10-266-090-13474

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| | | | | |
|---------------------------|-------|-------------------|----------|-------------|
| Query Match | 4.7% | Score 95.6 | DB 51 | Length 1069 |
| Best Local Similarity | 39.9% | Pred. No. 3.6e-06 | | |
| Matches 385; Conservative | 0 | Mismatches 489 | Totals 1 | Count 1 |

[illegible][illegible]

RESULT 10
US-10-473-126-240
: Sequence 340

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: sequence 240, application US/10473126
: GENERAL INFORMATION:
: APPLICANT: Epigenomics AG
: TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
: TITLE OF INVENTION: proliferative disorders
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/10/473,126
: CURRENT FILING DATE: 2003-09-26
: NUMBER OF SEQ ID NOS: 1258
: SEQ ID NO 240
: LENGTH: 8056
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: US-10-473-126-240

```

| | | | | |
|---------------------------|--------|--------------------|------------|--------------|
| Query Match | 4.5%; | Score 91.8; | DB 55; | Length 8056; |
| Best Local Similarity | 44.2%; | Pred. No. 2.4e-05; | | |
| Matches 627; Conservative | 0; | Mismatches 767; | Indels 25. | Gaps 0. |

| | | | |
|----|------|---|------|
| QY | 547 | AATGCTCTCAAAANGTTTTTAAATGCTAAATAATATGCCATCCAGATTAAGTAAATTT | 606 |
| Db | 1358 | ATTTTTTATTAATAAATTTATTTTTTTTTTATTAATAATAATATCGATTTTTTTTTATTTT | 141 |
| QY | 607 | CCCGTTTACCAGTTGTATAATATATGTTTTACCTTACAAGAGATATTCGTATACT | 666 |
| Db | 1418 | TTTATTTTTTTTTTTTTAAAAAAAATAAAAAATATTTTTTTTTTAATTAATATTTTAA | 1477 |
| QY | 667 | TTTAGACGACAGAGACTTAGTGCATAAATATGACGCTGTAAACACCTTAGCTGTGCA | 726 |
| Db | 1478 | ATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 1533 |
| QY | 727 | CTGTAAATTAAGTAATTTAGTATATAATAGTAGATCTACATAGACATTAATAATTAGA | 786 |
| Db | 1538 | TTTAATATTAATTAATTTTTTTTTAAAAAATTTATTTAATTTAATTTAATTTAATTTA | 1597 |
| QY | 787 | GCTATTAATTAAGTTCCTAATAAATAAGAGAGTTAGTAAACAGAAAGAGTAAAAACA | 846 |
| Db | 1598 | TAAATTTAATTTTAAAAAATCGAATAATACGAATCGTAAATTTAAAAAAATTAATTTT | 1657 |
| QY | 847 | AGAGCTTGCTGCTGTGTGTTAGTTAGTTGTGAGCTCATTTCTTTAAAGTAATGAAACT | 906 |
| Db | 1658 | AATTAATAC-GATTAATTTTATTTTATTTAATAATTAATAAATTAATTAATTAATAA | 1716 |
| QY | 907 | GATCTTAAGACATTAATAATTAAGTACAGGTTAAACTTTTACAAGAAATTAATTAAC | 966 |
| Db | 1717 | TATATATTATTAATTTTAATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 1776 |

| | | | |
|----|------|--|------|
| Qy | 967 | GAAATCACTTTTAATACATGCTCTCCGGCTGCAATTAATATAGGATCACTTACATGA | 1026 |
| Db | 1777 | AATTBAAAAATTATACGTATATATATTTTAATTTAATBAAATBAAAATTTTCGTTTA | 1836 |
| Qy | 1027 | TCGATTAAMACCTGTATAAA CAATTCATAGATBAAAATATCTTCAATGAAAAGAG | 1086 |
| Db | 1897 | AAAAATAAAAATTTTATATAAAAAAAATTAATATTAATATTAATTTTAAAAAATAT | 1956 |
| Qy | 1087 | GACATATGCTTTGAAAAAACAATAGTACTCCCTCCGCTCGAAATGTATACAT | 1146 |
| Db | 1897 | AAAAATAAAAATTTTATATAAAAAAAATTAATATTAATATTAATTTTAAAAAATAT | 1956 |
| Qy | 1147 | ATGATTTGCACGAGACATAGAAAAATGTATAAAGTATGTAGATBAAAAGAAAGAG | 1206 |
| Db | 1957 | AATTTTAAATTAATAATATTAATTAATTTTATTTBAAATTTAATBAAATTTTAAAT | 2016 |
| Qy | 1207 | A-----AGAAAAAGGGGTAAAGTACGGGAGCCACCAATATATTAATGATAGAT | 1256 |
| Db | 2017 | ATATTTAAATATAAATATATTTTAAAAATTTTATTTTAAAAAATTTTATTTAAAAAT | 2076 |
| Qy | 1257 | TTAGAAAAGTAGTTGAAAGTAGTGGGTGGGATTTTATATATTAATAAATTTACAT | 1316 |
| Db | 2077 | ATTTTAAATATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTAT | 2136 |
| Qy | 1317 | TTTGGAAAGTTTTCGAAATGTATAGAAATGTAGTGGGACATCATBAAAAGAAAGTATA | 1376 |
| Db | 2137 | TTTATTTAAAAATTAATAATTAATAATTAATAATTAATAATTTATTTTAAAAATTTAAAAA | 2196 |
| Qy | 1377 | GAAATTAATGGGACAGAGGAGTAAATCCTTATGATATATATAATTTTGTATTTTGAT | 1436 |
| Db | 2197 | ACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 2256 |
| Qy | 1437 | TTTCATTAAGATATATAATCTAGTTATAAGATATATAATTTTAAAAATATACATAT | 1496 |
| Db | 2257 | TTTAAAAATTAATTAATAAATAATTTTAAATTTTATTAATTTATTAATTTTAAAAATTAAT | 2316 |
| Qy | 1497 | AATTCGATTAATGCGATTAACCGCCTTTATATATTTTACATACTAGATTAATGAAATAA | 1556 |
| Db | 2317 | AATTTTGGTATTAATTAATTTTATTTTAAATTTTAAATAATATTTTATTTTATTAATAA | 2376 |
| Qy | 1557 | TCAGTATCTGAAAAGCAAT-----AATATCTTTGTAACAGCGTTCGTCGAATGG | 1610 |
| Db | 2377 | TAAATTTATTAATTTTATTTATTTTTCGAAAAATTAATAAATAAATAATTAATTTATTTTAA | 2436 |
| Qy | 1611 | GAAGTCACTGATCAATCAATAGTTTATATBAAAAGTAAATTTTAAAT-----AATGTT | 1666 |
| Db | 2437 | AAAAATTAATTTTATTTTATTTTATTTTATTAATTAATTTTATTAATTTTATTAATTTTAT | 2496 |
| Qy | 1667 | ATTTTGTGTTTCAGAAATTTTAAATTAATTAATTTAGACATGGAGATTCACGGCATCATG | 1726 |
| Db | 2497 | AAAAATTAATTAAGAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 2556 |
| Qy | 1727 | AGCAGCACTAGACGTGTTGAAACAATGTATGTCCGGGTGACATCTATGACCTTTCACTCA | 1786 |
| Db | 2557 | AAAAATTTAAATTAATTTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 2616 |
| Qy | 1787 | AATAGTGAATTAATGATCTTAGAATACATCTTTTCAAAATTTCAACAAACACAGCTTTAA | 1846 |
| Db | 2617 | AATATATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 2676 |
| Qy | 1847 | CTTTTCTTTCAACGAGATGGAATCCYTTCTBAACTTTTAAATTAATAAATAAATGACATTA | 1906 |
| Db | 2677 | AT-----TTTTAAATTTTATTTTAAATTTATTTTATTTTATTTTAAAAAATAATTCGTTA | 2732 |
| Qy | 1907 | TTGTATATTTTATGACACCTCAACATGTAGCTAGCGT | 1945 |
| Db | 2733 | AATATAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA | 2771 |

RESULT 11
US-10-473-126-386/c
; Sequence 386, Application US/10473126

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? GENERAL INFORMATION:
? APPLICANT: Epigenomics AG
? TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
? TITLE OF INVENTION: proliferative disorders
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/10/473,126
? CURRENT FILING DATE: 2003-09-26
? NUMBER OF SEQ ID NOS: 1258
? SEQ ID NO 386
? LENGTH: 8056
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match          4.5%; Score 91.6; DB 55; Length 8056;
Best Local Similarity 46.1%; Pred. No. 2 6e-05;
Matches 455; Conservative 0; Mismatches 524; Indels 9; Gaps 4;

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| Query Match | 4.5% ; Score 91.6 ; DB 55 ; Length 8056 ; |
|-----------------------|--|
| Best Local Similarity | 46.1% ; Pred. No. 2, 6e-05 ; |
| Matches 455 ; | Conservative 0 ; Mismatches 524 ; Indels 9 ; Gaps 4 ; |
| Qy 732 | AAATAGATTAATTTGGTAGATTAATATAGTAGATCTACAAATGACCTTAATAATTAGACTAT 791 |
| Dy | AAAAATAAAATAATTTTATTAATTTTAAAAATTAATATATATATATCAAAATTTAAAAAT 7496 |
| Qy 792 | TAATTAAGTACATTAATAATTAAGAGAGTATAGTAAAGAAAGAGGTAATAACAAGAC 851 |
| Dy | TATATATTTTATTTTAAATATTTAAACATTTAAATTAATTAATTAACAAATTAATTAATTT 7436 |
| Qy 852 | TTGCTGCTGTGTGTTTATGTTTGTGTGACTATTTCTTTAAAGTAATGTAACTGATCT 911 |
| Dy | TAATATACATATATATATATATATACATATTTTTTTTTTCAATATATTTTTTTTTTAAAA 7376 |
| Qy 912 | AAAGCATATGAAATTTAGTACAGGTTAAACCTTTACAAAGATTTATTTAAACGAAA 971 |
| Dy | TAAT 7316 |
| Qy 972 | TCATTTATATACATATGCTCTCGGCTGTCAATATA-ATAGGATCAGCTTACATCATCCA 1030 |
| Dy | AAATATTTTTTATTTTTTATATATATCAATAAATATATATATATATATATATATATAT 7256 |
| Qy 1031 | TTTAAACCTTGTATTAACAAATTCMATGAGATTAATAATATCTTCAATGAAAGAGACA 1090 |
| Dy | ATATATATATATTAATAATTAATATATTTTTTAAATAATATATATATATATATATAT 7196 |
| Qy 1091 | ATGCTCTTTGAAAAAAACAATATAGTACTCCCTCCGCCCTCTGAAATGTATACATATG 1156 |
| Dy | AAATTAATTAATATCAAAACATTAATTAATAATTAATATATATATATATATATATAT 7136 |
| Qy 1151 | ATTGACACGAGACTAAGAAAAATGTATTAAGTATGTAGAGTAAAGAAAGAAAGAAAG 1210 |
| Dy | TATTTTAT 7078 |
| Qy 1211 | AAAAGTGGTAAAGTAGCGGAGCCACCAATATATTAATGTATGATTTAGAAAATGATT 1270 |
| Dy | AAAAATTAATTAATTTTAAATTTTAAATTTTTTTTTTTTTTAAAAAAATCAAAA 7018 |
| Qy 1271 | GAAAGTGGGAGGAGGAGATTTTATATTAATTAATAATTTACATTTTGGAAGTTT 1330 |
| Dy | TATATTTTTTTTTTTTTTTTTTAAATCAATATATTTTTTATATATATATATATAT 6958 |
| Qy 1331 | GAAATGTATAGAAATGTAGTGGAGCATCATTAAGAAAGAAAGTATAGAAATTAATGGGAC 1390 |
| Dy | TTAT 6898 |
| Qy 1391 | AGAGGAGTATACCTTATGATATATATATATTTTTTGTATTTGATTCATATAGATATA 1450 |
| Dy | AAAAAAATTAACATTTTTTTTTTATATATATATATATATATATATATATATATATAT 6838 |
| Qy 1451 | AATCTATGTATATATGAT 1506 |
| Dy | ATTTTTTATATATATTTTTTTTTTAAATAATCAATTTTCAATTCATATATATATAT 6778 |
| Qy 1507 | AGTCGATTAACGCCCTTTATATATTTTACAACTAGTAAATATAGATTAATACGTTATCT 1566 |

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Db      6777 TTTATATTTTTCATTATTAATTTT- -AATTTTTTAAATTCATATTCATAAATATAT 6720
Qy      1567 GAAAGCAATATATATCTTGTAAACAGCGTTCGTCATAATGGAGTCAATGTAT 1626
Db      6719 TATTAATCAACATTAATAAACAATAAAAAAATTTATTTTAAATTAATTAATAA 6660
Qy      1627 CAATAGTTTAAATATATAAGTAATTTAAATTAATTTTATTTTGTTCAGAAATTTA 1686
Db      6659 TTTAAATTTTCATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 6600
Qy      1687 AATATAATTTGAGCATGGAGTCA 1714
Db      6599 AATATAATTTTTCATTTAATTTAA 6572

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RESULT 12
US-09-806-197-2/c
; Sequence 2, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NISHIKAWA, SATOMI
; APPLICANT: OEDA, KENJI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-2

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Query Match
Best Local Similarity 4.3%; Score 88.6; DB 35; Length 851;
Matches 221; Conservative 0; Mismatches 119; Indels 31; Gaps 3;

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Qy      3 TGTGTCCCTACAGACATAGGCGCTGTGTGTGAGAGAGAGAGAGAGAGAGTCTGACT 62
Db      715 TGTGTGTCTCTCTCATTTAGATTAACATCTTATAGAGAGTACCTCCAGCTTTTGTCT 656
Qy      63 TCTTCTCTTTGACCTTTTGTATTAAGAGT-AGAAATATTTTAAAGAGTGGAGT 121
Db      655 TCCACTTTCCTTGACCGCTTGTGTAAAGAGTAAAGAGTCTTTAAGAGCGTGA 596
Qy      122 ACTAATCTC-----TCTCAACAATTCGCTTCTTTTCCAAACA 161
Db      595 AATAGTTGAAGTAAAGAAATGCTAAGTCTTTTCAACTCTATTTCTTTTCCAAACA 536
Qy      162 CTTTATTAAGT-----TTTACTTCTCATTTTACTCACTCTTTGTCTATAG 211
Db      535 CTTTATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 476
Qy      212 CAAGAAATCACTCTTTTAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
Db      475 TAAAGAGTCACTTTTAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Qy      272 TATCTTCAATTTAGATTAACAATAGTGAACAGAGTATTTTAAAGTGAAGAGAG 331
Db      415 ACTTATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 356
Qy      332 TTTCTAATTAAT 342
Db      355 TTTCTCTTANT 345

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RESULT 13
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; GENERAL INFORMATION:
; APPLICANT: Bpigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell

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; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

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Query Match
Best Local Similarity 4.3%; Score 88.6; DB 55; Length 8056;
Matches 442; Conservative 0; Mismatches 519; Indels 12; Gaps 3;

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Qy      736 AGATAATGTGTAGTAAATATAGTATGATCTACATGACATTAATTAAGCTATTAAT 795
Db      1399 ATATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1340
Qy      796 TAAGTATCTAATTAATTAAGAGGTTAGTAACAGAAAGAGTAAACAGAGCTTGC 855
Db      1339 TATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1280
Qy      856 TCGTGTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 915
Db      1279 TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1220
Qy      916 CACATGAATTTTGTACAGGTTAAACCTTTACAGAAATTAATTAATTAATTAATTAAT 975
Db      1219 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1160
Qy      976 TTTAAACATGTCTCTCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1035
Db      1159 TTAATTTTAAATTTTGAATATGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1100
Qy      1036 ACCTTGTAAACAAATCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1095
Db      1099 AAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1040
Qy      1096 TCTTTGAAAAAACAATTAAGTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1155
Db      1039 AATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 980
Qy      1156 ACAGAGAGCTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1215
Db      979 TTTTATTCGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 920
Qy      1216 TGGGTAAAGTACGCGGACCAACAATTAATTAATTAATTAATTAATTAATTAATTA 1275
Db      919 GACGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 860
Qy      1276 TAGGTGGTGGGAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1334
Db      856 TAAAAAACAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 800
Qy      1335 TGTATAGATTAAGTGGAGATCAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1394
Db      799 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 740
Qy      1395 GAGATTAATCCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1448
Db      739 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 680
Qy      1449 TAAATCTATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1508
Db      679 TTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 620
Qy      1509 TCGATTAACGCTTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1563
Db      619 TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 560

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[illegible]

Search completed: March 15, 2005, 17:31:32
Job time : 7607.94 secs


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/ Sequence 568, Application US/10517441
/ GENERAL INFORMATION:
/ APPLICANT: FOKENS, John
/ APPLICANT: HARBEC, Nadia
/ APPLICANT: KOENIG, Thomas
/ APPLICANT: MAIER, Sabine
/ APPLICANT: MARTENS, John
/ APPLICANT: MODEL, Fabian
/ APPLICANT: NIMMICH, Inko
/ APPLICANT: RUJAN, Tamas
/ APPLICANT: SCHMITT, Armin
/ APPLICANT: SCHMITT, Manfred
/ APPLICANT: LOOK, Maxime P.
/ APPLICANT: MARX, Almut
/ APPLICANT: HOEPLER, Heinz
/ TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
/ FILE REFERENCE: 47675-93
/ CURRENT APPLICATION NUMBER: US/10517,441
/ PRIOR FILING DATE: 2004-12-11
/ PRIOR APPLICATION NUMBER: PCT/EP2003/010881
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: DE 10317955.0
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: DE 1030096.8
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: DE 10245779.4
/ PRIOR FILING DATE: 2002-10-01
/ NUMBER OF SEQ ID NOS: 2147
/ SEQ ID NO 568
/ LENGTH: 5286
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-568

Query Match      3.5%; Score 70.8; DB 7; Length 5286;
Best Local Similarity 44.6%; Pred. No. 0.00017;
Matches 358; Conservative 0; Mismatches 442; Indels 2; Gaps 2;
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896 TATGTAACTGATCTTAAGACATAGAAATTTAGTACAGTTAAACCTTTTACAAGAAAT 955
4883 TATTAATATATATATATATATATATATATATATATATATATATATATATATATAT 4824
956 TTAATATTAAGAAATCATTTTATTAACATGCTCTCGCTGCTATTATATATGAGATCA 1015
4823 TATTATATTAACAATATATATATATATATATATATATATATATATATATATATATTA 4764
1016 CTACATGATCCATTAACCTTTTAAACAAATTCAGATGATTAATAATCTTACA 1075
4763 TATA-TTATATATATATATATATATATATATATATATATATATATATATATATATTA 4705
1076 ATGAAAGAGAGACATGCTCTTTGAAAAACAATAGGTAAGTCCCTCCGCTCTGA 1135
4704 TTAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4645
1136 AATGATACATATGATGAGACGAGACTAAGAAAAATGATTAAGTATGAGTA 1195
4644 TATATATATATATATATATATATATATATATATATATATATATATATATATATATTA 4585
1196 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1255
4584 TATTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 4525
1256 TTTAGAAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1315
4524 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4465
1316 TTTGAGAAAGTTTGAATGATAGAAATGAGTGGAGACATCCATTAAGAGAGAGAGTA 1375
4464 TTAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4405
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Qy 1376 AGAATTAAGTGGACAGAGAGATATACCTTTATGATATATATATATATATTTGTTATTTGA 1435
Db 4404 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4345
Qy 1436 TTTGATAGATATATATATATATATATATATATATATATATATATATATATATATATAT 1495
Db 4344 TATTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 4285
Qy 1496 TAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1555
Db 4284 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4226
Qy 1556 ATCAGTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1615
Db 4225 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4166
Qy 1616 TCAATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 1675
Db 4165 TTAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 4106
Qy 1676 TCAAGAAATTTAAATTAATTAAT 1697
Db 4105 ATTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 4084
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RESULT 4
US-11-033-545-592
/ Sequence 592, Application US/11033545
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
/ TITLE OF INVENTION: AND USES THEREOF
/ FILE REFERENCE: CL000790
/ CURRENT APPLICATION NUMBER: US/11/033,545
/ PRIOR FILING DATE: 2005-01-12
/ PRIOR APPLICATION NUMBER: 60/231,401
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 10823
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 592
/ LENGTH: 18651
/ TYPE: DNA
/ ORGANISM: Human
US-11-033-545-592

Query Match      3.3%; Score 68.4; DB 8; Length 18651;
Best Local Similarity 48.8%; Pred. No. 0.00053;
Matches 250; Conservative 0; Mismatches 251; Indels 11; Gaps 2;
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Qy 1201 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1260
Db 9943 ATAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 10002
Qy 1261 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1320
Db 10003 AATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10062
Qy 1321 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1380
Db 10063 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10122
Qy 1381 TAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1440
Db 10123 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10173
Qy 1441 TAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Db 10174 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10231
Qy 1501 CTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 10232 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10291
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APPLICANT: HO

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RESULT 9
US-10-517-441-568
; Sequence 568, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FORTKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: ROUAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFLE, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cells

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| | | | | | |
|-----------------------|--------------|--------------------|-----------------|--------------|--------|
| Query Match | 3.3% | Score 67; | DB 7; | Length 5286; | |
| Best Local Similarity | 44.7%; | Pred. No. 0.00088; | | | |
| Matches 450; | Conservative | 0; | Mismatches 535; | Indels 22; | Gaps 4 |

[illegible]

RESULT 10
US-60-655-875-1533/c
; Sequence 1533, Application US/60655875

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: GENERAL INFORMATION:
: APPLICANT: Boukharov, Andrey
: APPLICANT: Du, Zifeng
: APPLICANT: Guo, Liang
: APPLICANT: Kovalic, David
: APPLICANT: Lu, Maolong
: APPLICANT: McCarter, James
: APPLICANT: Miller, Nancy
: APPLICANT: Williams, Deryck
: APPLICANT: Vaudin, Mark
: APPLICANT: Wu, Wei
: TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
: TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
: FILE REFERENCE: 38-21(53885)
: CURRENT APPLICATION NUMBER: US/60/655,875
: CURRENT FILING DATE: 2005-02-24
: NUMBER OF SEQ ID NOS: 171306
: SEQ ID NO 1533
: LENGTH: 3999
: TYPE: DNA
: ORGANISM: Heterodera glycines
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (3918)..(3918)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (3946)..(3946)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (3964)..(3964)
: OTHER INFORMATION: n is a, c, g, or t
: US-60-655-875-1533
:
: Query Match 3.2%; Score 66; DB 9; Length 3999;
: Best Local Similarity 49.3%; Pred. No. 0.0013;
: Matches 201; Conservative 0; Mismatches 205; Indels 2; Gaps 1;
:
Oy 1286 GTGGATTATTAATTAATAAAATTACTATTTGAGAAAGTTTGAATGTATAGATT 1345
Db 893 GGGGGATTTTATTTTAAATATATTTCTAAATTTTATCTATCTTGATTTTAGCGGATA 834
Oy 1346 GAGTGGGACATCCATTAAGAAGATGTATAGATTAAATGGAGCAGAGGAGTAAATCC 1405
Db 833 AAATATTAATAATGAATGAGAGAGATTTTCTAATTTAAGTAATTAATTAATATTTT 774
Oy 1406 TTATGATATTAATTTTGTCTATTTTGATTTCAATAGATTAAATCTATGTTATAT 1465

```

Db 773 TTCA--ATCCTGCATTTTTTTTGGATGGAATGATAAAGATTTAATGAAATGAGAAC 716
Qy 1466 GATAATATATATTTTAAAAATATCTATATTAATTCGATTAGTCGATACGCCCTTTTA 1525
Db 715 TTTCTAATTAATATATATATGAAAAATTTATTTTAAATTTTATTTTTCGATTTTAA 656
Qy 1526 TAAATTTTACATCTGAGTAATATGAAATTAATCAGTTATCGAAGAACAAATATATCTT 1585
Db 655 TTGAAATTAATAAAATATATTAATTAATTAAGGTTTCTATCCGGAAATCAAAAAATTT 596
Qy 1586 TGTAAAAACGGCTTCGTCGAATGGAAGTTCAATGTATTTCAATAGTTTAAATATATAA 1645
Db 595 TAAGAGAAAAATCCTTTTTCATGAGTATATTTCAATACATATTTAATTTTTCCTCAATCA 536
Qy 1446 GTAATTTTAAATTAATTTGTTATTTTGTTCAGAAATTTTAAATTA 1693
Db 535 TGTATATTTTCAATGTTTAAATTTTGTAAATAAGAAAAATTTTAA 488

RESULT 11
US-10-517-441-24
; Sequence 24: Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOERKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NITWIRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 24
; LENGTH: 5286
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-517-441-24

Query Match 3.2%; Score 65.4; DB 7; Length 5286;
Best Local Similarity 44.9%; Pred. No. 0.0017;
Matches 450; Conservative 0; Mismatches 546; Indels 7; Gaps 5;
Qy 917 ACATGAAATTTAGTACAGGTAAACCTTTACAGAAATTTATTTAAACGAAATCATT 976
Db 66 ATATATAAAATATGTAAT 125
Qy 977 TTATAACATGCTCTCGCGCTGATATATATATAGGAGTCACTACT-GATCATTCAATTA 1035
Db 126 ATATATAATGAT 185
Qy 1036 ACCTGTTTAAACAAATTCATGAGATTAATATATCTTACATGAAAGAGAGCAATGTC 1095
Db 186 TGTAT 245
Qy 1096 TCTTTGAAAAAACAATATAGTACTCCCTCCCTCTGAAATGATATACATATGGAATTGG 1155

Db 246 ATTAT 305
Qy 1156 ACACGAGACTAAGAAAAATGTAATAAGTATAGTAGTAAGAAAAAGAAAAAG 1215
Db 306 TAT 365
Qy 1216 TGCGTAAGTAGCGGAGCCACCAATATATATATATATATATATATATATATATATAT 1275
Db 366 ATATATAATGAT 425
Qy 1276 TAGTGGCGGCGGAGATTTTATATATATATATATATATATATATATATATATATAT 1334
Db 426 TAT 485
Qy 1335 TGTATAGAAATGAGTGGACATCCATTAAGAAAGAAATGATATAGAAATTAATGGA 1394
Db 486 TGTAT 545
Qy 1395 GGAGTATACCT-TTATGATATATATATATATATATATATATATATATATATATAT 1453
Db 546 TGTAT 605
Qy 1454 CTATGTTATATGAT 1513
Db 606 AATGCTAT 665
Qy 1514 TACCGCTTTTAAATTTTACAAATCTGAGTAATATGAAATCACTTATCTGAAAGC 1573
Db 666 TGTAT 722
Qy 1574 AATATATATCTTGTAAAAACGCGTTCGTAATGGAAGTTCATGCTATCAATGCT 1633
Db 723 GTAT 782
Qy 1634 TTTAT 1692
Db 783 TAT 842
Qy 1693 ATTATGAGCATGGAGATTCACGGGATCATGAGCAGCACTAGACTGTTGAAACATG 1752
Db 843 ATTAT 902
Qy 1753 TATGTCGGGTGATCATCTAGACCTTCACTCAACCTAGGAATATGATCTAGAAAT 1812
Db 903 TAT 962
Qy 1813 ACATCTTTCAAAATTTCAACAAACAGCTTAACTTTCTTCAACGATGGAATCCT 1872
Db 963 AT 1022
Qy 1873 TTTCAAACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1915
Db 1023 TAT 1065

RESULT 12
US-10-932-182A-166179/C
; Sequence 166179: Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIRO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166179
; LENGTH: 8391

TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166179

Query Match 3.1%; Score 64.6; DB 6; Length 8391;
Best Local Similarity 45.8%; Pred. No. 0.0025;
Matches 302; Conservative 0; Mismatches 349; Indels 8; Gaps 2;

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QY 1042 TTAACCAATTCATGATGATTAATATCTTACATGAAAGAGACATGCTCTTGG 1101
DB 1017 TTAATTAATATATATGATATATATACCTGTATAGTTTAATGGTTAAACATTTGTC 958
QY 1102 AAAAAACAATAGTATCTCCCTCCCTCTGAAAATGATACATATGATGATGGACACG 1161
DB 957 ATAAATTAATATATGATGATGATCAATTCCTCTCAAGATATATATATATATATATAT 898
QY 1162 AGACTAAGAAAAATGATATATGATGATGATGATGATGATGATGATGATGATGATG 1221
DB 897 ATAAATTAATATATATATATATATATATATATATATATATATATATATATATAT 838
QY 1222 AAGTAGCGGACCCACCATATATATATGATGATGATGATGATGATGATGATGATG 1281
DB 837 TAATATATGATATATATATATATATATATATATATATATATATATATATATAT 778
QY 1282 GTGGGTGGATTTTATATATATATATATATATATATATATATATATATATATAT 1341
DB 777 GTCCCTAGGACCCGATATATATATATATATATATATATATATATATATATATAT 723
QY 1342 AATTGATGGACATCCATTAAGAAAGATGATGATGATGATGATGATGATGATGAT 1401
DB 722 TAAATTTTAAATATATATATATATATATATATATATATATATATATATATAT 663
QY 1402 TACCTTATGATATATATATATATATATATATATATATATATATATATATAT 1461
DB 662 AATATTTTAAATATATATATATATATATATATATATATATATATATATATAT 603
QY 1462 TATGATATATATATATATATATATATATATATATATATATATATATATATAT 1521
DB 602 TAAATTAATATATATATATATATATATATATATATATATATATATATATATAT 543
QY 1522 TTTATATATTTTACATATCTGATATATGATATATATATATATATATATATAT 1581
DB 542 TTAATTAATATATATATATATATATATATATATATATATATATATATATATAT 483
QY 1582 TCTTTGTAAACAGCGCTTGGCTCAATGGAGATCATGTGATCATATAGTTTAAAT 1641
DB 482 TAAAAAAGAGATATATATATATATATATATATATATATATATATATATATAT 423
QY 1642 AAAAAATATTTTAAATATATATATATATATATATATATATATATATATATAT 1700
DB 422 AA---TAATTAATATATATATATATATATATATATATATATATATATATATAT 367

```

RESULT 13
US-10-517-441-564

Sequence 564, Application US/10517441

GENERAL INFORMATION:
APPLICANT: FOKKENS, John
APPLICANT: HARBEC, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARK, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
FILE REFERENCE: 47675-93

CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 564
LENGTH: 16579
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)

Query Match 3.1%; Score 64.6; DB 7; Length 16579;
Best Local Similarity 45.5%; Pred. No. 0.0027;
Matches 229; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

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QY 1176 GTATAAGTATGTAGATTAAGAAAGAGAAAGAAAGAGAAAGAGAAAGAGAAAG 1235
DB 4214 GAAGAAATATTGTATAGTAGAGAAATATATGATTTAGGTGAAATTTATGAAAT 4273
QY 1236 ACCATATATATATGATATATATTAAGAAAGATGTAAGATGATGATGATGATGAT 1295
DB 4274 TATTTTATTAAGATATATATATATATATATATATATATATATATATATATAT 4333
QY 1296 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 1355
DB 4334 TATATTTGTTTATATATATATATATATATATATATATATATATATATATATAT 4393
QY 1356 TCCATTAAGAAAGATGTATAGATTAAGAAAGAGAAAGAGAAAGAGAAAGAT 1415
DB 4394 TTAATTAAGATATATATATATATATATATATATATATATATATATATATATAT 4453
QY 1416 ATAAATTTTGTATTTTATATATATATATATATATATATATATATATATATAT 1475
DB 4454 ATATATATATTTGTATATATATATATATATATATATATATATATATATATAT 4513
QY 1476 TTTTAAATATATATATATATATATATATATATATATATATATATATATATAT 1535
DB 4514 TAATAGAGATTTTGTATGTTTGTATATATATATATATATATATATATATATAT 4573
QY 1536 ATACTGAGTATATATATATATATATATATATATATATATATATATATATATAT 1595
DB 4574 TAAATATTTGTTTAAAGAAATATATATATATATATATATATATATATATATAT 4633
QY 1596 CGTTCGTCAAATGGAGATCATGTATATATATATATATATATATATATATATAT 1655
DB 4634 ATTAGTTTATATATATATATATATATATATATATATATATATATATATATAT 4693
QY 1656 AATTAATTTGTATATTTTGTATCA 1678
DB 4694 AATTAGTAATATATATATTTTATTA 4716

```

RESULT 14

US-60-655-875-7091/C

Sequence 7091, Application US/60655875

GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey
APPLICANT: Du, Zifeng
APPLICANT: Guo, Liang
APPLICANT: Kovalic, David
APPLICANT: Lu, Maolong
APPLICANT: McCarter, James
APPLICANT: Miller, Nancy
APPLICANT: Williams, Deryck
APPLICANT: Vaudin, Mark

```

? APPLICANT: Wu, Wei
? TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
? TITLE OR INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
? FILE REFERENCE: 38-21(53885)
? CURRENT APPLICATION NUMBER: US/60/655,875
? CURRENT FILING DATE: 2005-02-24
? NUMBER OF SEQ ID NOS: 171306
? SEQ ID NO 7091
? LENGTH: 2421
? TYPE: DNA
? ORGANISM: Heterodera glycines
? US-60-655-875-7091

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| | | | | |
|-----------------------|--------------|-------------------|-----------------|--------------|
| Query Match | 3.1%; | Score 63.2; | DB 9; | Length 2421; |
| Best Local Similarity | 49.5%; | Pred. No. 0.0041; | | |
| Matches 190; | Conservative | 0; | Mismatches 193; | Indels 1; |
| | | | Gaps | 1; |

| | | | |
|----|------|--|------|
| QY | 730 | ATTAATATGATTAATGTTAGTAAATGAAATGAGATCTACATGACATTAATATGAGCT | 189 |
| Db | 889 | ATAAAAATAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 830 |
| QY | 790 | ATTATATTAGTCTACTAATATAATTAAGAGAGGTTAGTAAACAGAAAGCGTAAAAACAGA | 849 |
| Db | 829 | TTAAAAATPAATTTAAAAATTAATAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA | 770 |
| QY | 850 | GCTTGCTGCTGCTGCTTGGTTGAGCTCATTTCTTTAAAAAGTAAGTAAACATGAT | 909 |
| Db | 769 | ATAAAAATPAATTTAAAAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAATTA | 710 |
| QY | 910 | CTAAGACACATAGAAATTTAGTACAGGTTAAACCTTTACACAGATTTATATTAAAAAGAA | 969 |
| Db | 709 | ATATAAAATTAATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 651 |
| QY | 970 | AATCATTTTATACATGCTCTCGGCTGTCATTAATAATAGGATCATCTTACTGATCCTC | 1028 |
| Db | 650 | AATTAATAATTAATAATTAATTAATTTAAATTAATAATTAATAATTAATAATTAATAATTA | 591 |
| QY | 1030 | ATTAAAAACCTTGTAAAAACAATTCCATGAGATAAAAATCTTACATGAAAAAGAGAC | 1089 |
| Db | 590 | AATTAATAATTAATAATTAATAATTTAAAAATTAATAATTAATAATTAATAATTAATAATTA | 531 |
| QY | 1090 | AATGCTCTTTGAAAAACAAATA 1113 | |
| Db | 530 | AATAAAAATTAATTTAAATTAATA 507 | |

```

1      RESULT 15
2      US-10-517-441-290
3      ; Sequence 290, Application US/10517441
4      ; GENERAL INFORMATION:
5      ; APPLICANT: FOEKENS, John
6      ; APPLICANT: HARBECK, Nadia
7      ; APPLICANT: KOENIG, Thomas
8      ; APPLICANT: MATER, Sabine
9      ; APPLICANT: MARTENS, John
10     ; APPLICANT: MODEL, Fabian
11     ; APPLICANT: NIMMERICH, Inko
12     ; APPLICANT: RUJAN, Tamas
13     ; APPLICANT: SCHMITT, Armin
14     ; APPLICANT: SCHMITT, Manfred
15     ; APPLICANT: LOOK, Maxime P.
16     ; APPLICANT: MARX, Almut
17     ; APPLICANT: HOFFER, Heinz
18     ; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cancer
19     ; TITLE OF INVENTION: proliferative disorders
20     ; FILE REFERENCE: 47675-93
21     ; CURRENT APPLICATION NUMBER: US/10/517,441
22     ; CURRENT FILING DATE: 2004-12-11
23     ; PRIOR APPLICATION NUMBER: PCT/EP2003/010861
24     ; PRIOR FILING DATE: 2003-10-01
25     ; PRIOR APPLICATION NUMBER: DE 10317955.0
26     ; PRIOR FILING DATE: 2003-04-17
27     ; PRIOR APPLICATION NUMBER: DE 10300096.8

```

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? PRIOR FILING DATE: 2003-01-07
? PRIOR APPLICATION NUMBER: DE 10245779.4
? PRIOR FILING DATE: 2002-10-01
? NUMBER OF SEQ ID NOS: 2147
? SEQ ID NO 290
? LENGTH: 16579
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-290

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| | | | | |
|-----------------------|-----------------|-------------------|-----------|---------------|
| Query Match | 3.1%; | Score 63; | DB 7; | Length 16579; |
| Best Local Similarity | 45.3%; | Pred. No. 0.0053; | | |
| Matches 228; | Conservative 0; | Mismatches 275; | Indels 0; | Gaps 0; |

| | | | |
|----|------|---|------|
| QY | 1176 | GTATTAAGTAAATGTAAGGTAAAGAAAGAAAGAAAGAAAGGCGGTAAAGTATGCGGACCC | 1235 |
| Db | 4214 | GAAAGAAATTATGTAATGTAAGTAAGAAATTAACGCAATTTAGTGCGAATTTATGAAATT | 4273 |
| QY | 1236 | ACCAATATATATGATGAGATTAGAAAAGTAGTTGAAAGTAGTGGGTGGGTGGCAATTTT | 1295 |
| Db | 4274 | TATTTTATATAGTAATAGTATATATGCAATTTTGAATTTGGATTTGGTTAAGTTT | 4333 |
| QY | 1296 | TATTTTATTAATAATTTCTATTTTGGAGAAAGTTTGAAGATGATAGATAGAGATGAGGACA | 1355 |
| Db | 4334 | TATATGTCCGTTTATAGATATTTTTTTGTTTTTTTGTGGTGGAATTTTTTTTTTATATAT | 4393 |
| QY | 1356 | TCCATTAAGAAAGAAAGTGTATGAAATTAATGGAACAGAGGAGTAATACCTTATGATAT | 1415 |
| Db | 4394 | TTATTTTAAGATATCTGTATTTTTTTTTTTTTTTTAAAGTTTTTATTTTTATTTTTAGTATAT | 4453 |
| QY | 1416 | ATAATATTTTGTATTTTGAATTCATATAGATTAATAATCTATGTTATATAGATATATATA | 1475 |
| Db | 4454 | ATTATATTTTGTATATATGTAATGGAATGTTTTTTTTTATTTATTTATATATAGTAAAGTTT | 4513 |
| QY | 1476 | TTTTTAAATAATATCTATATTAATTCGATTATGCAATTAACCGCTTTATATTAATTTACA | 1535 |
| Db | 4514 | TAAATAGAGTAGTTTTTATGTTTTGTTTATTTTTTGTATTTAATGTTTAAAGAAATATTAG | 4573 |
| QY | 1536 | ATATCTGAGTAATATGAAATTAATTCGTTATCTGAAAGCAATATATATCTTTGTAAACAG | 1595 |
| Db | 4574 | TAAATATTTTGTAAAGATGCAATATATATTTATTTATATTAATTAAGATGATATATATAT | 4633 |
| QY | 1596 | CGTTCCGTCAAATGGAAGTTCAATGTGTATTCAAATAGTTTAAATATTAAGTAAATTTTA | 1655 |
| Db | 4634 | ATTATAGTTTATATTAATATTTTTTTTATTTATAGATATTAATATTTTGGAGAAATGTTTTA | 4693 |
| QY | 1656 | AATTAATTTGTAATTTTGTCTCA | 1678 |
| Db | 4694 | AATTAATTAATATATATTTTTTTA | 4716 |

Search completed: March 15, 2005, 18:04:55
Job time : 1980.74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: March 15, 2005, 08:26:53 / Search time 386.236 seconds
(without alignments)
8693.245 Million cell updates/sec

Title: US-09-806-197-1

Perfect score: 2052

Sequence: 1 catgtgtgcctcacagcaca.....gcaatacatcttaataatc 2052

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
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6: /cgn2_6/prodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 241.2 | 11.8 | 2042 | 2 | US-08-911-434A-2 |
| 2 | 196.6 | 9.6 | 247 | 2 | US-08-911-434A-1 |
| 3 | 195.6 | 9.5 | 246 | 3 | US-09-352-608-2 |
| 4 | 119 | 5.8 | 140 | 3 | US-09-352-608-6 |
| 5 | 119 | 5.8 | 140 | 3 | US-09-352-608-7 |
| 6 | 81.4 | 4.0 | 187169 | 4 | US-09-949-016-12776 |
| 7 | 81.4 | 4.0 | 191569 | 4 | US-09-949-016-15940 |
| 8 | 72.2 | 3.5 | 205044 | 4 | US-09-949-016-15851 |
| 9 | 72.2 | 3.5 | 205044 | 4 | US-09-949-016-15852 |
| 10 | 72.2 | 3.5 | 205044 | 4 | US-09-949-016-15853 |
| 11 | 72.2 | 3.5 | 223471 | 4 | US-09-949-016-12387 |
| 12 | 72.2 | 3.5 | 223471 | 4 | US-09-949-016-12724 |
| 13 | 72.2 | 3.5 | 223471 | 4 | US-09-949-016-12725 |
| 14 | 69.4 | 3.4 | 7218 | 1 | US-08-232-463-14 |
| 15 | 68.6 | 3.3 | 1141 | 4 | US-09-806-708B-22 |
| 16 | 68.6 | 3.3 | 18773 | 4 | US-09-949-016-14164 |
| 17 | 68.2 | 3.3 | 1141 | 4 | US-09-806-708B-22 |
| 18 | 67.8 | 3.3 | 205044 | 4 | US-09-949-016-15851 |
| 19 | 67.8 | 3.3 | 205044 | 4 | US-09-949-016-15852 |
| 20 | 67.8 | 3.3 | 205044 | 4 | US-09-949-016-15853 |
| 21 | 67.8 | 3.3 | 223471 | 4 | US-09-949-016-12387 |
| 22 | 67.8 | 3.3 | 223471 | 4 | US-09-949-016-12724 |
| 23 | 67.8 | 3.3 | 223471 | 4 | US-09-949-016-12725 |
| 24 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-30530 |
| 25 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-30531 |
| 26 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-37149 |
| 27 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-37150 |

| | | | | | | |
|----|------|-----|--------|---|----------------------|--------------------|
| 28 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-37163 | Sequence 37163, A |
| 29 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-37164 | Sequence 37164, A |
| 30 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-145867 | Sequence 145867, A |
| 31 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-145868 | Sequence 145868, A |
| 32 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-146135 | Sequence 146135, A |
| 33 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-146136 | Sequence 146136, A |
| 34 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-146403 | Sequence 146403, A |
| 35 | 67.2 | 3.3 | 601 | 4 | US-09-949-016-146404 | Sequence 146404, A |
| 36 | 67 | 3.3 | 601 | 4 | US-09-949-016-30531 | Sequence 30531, A |
| 37 | 67 | 3.3 | 601 | 4 | US-09-949-016-37150 | Sequence 37150, A |
| 38 | 67 | 3.3 | 601 | 4 | US-09-949-016-37164 | Sequence 37164, A |
| 39 | 67 | 3.3 | 601 | 4 | US-09-949-016-145868 | Sequence 145868, A |
| 40 | 67 | 3.3 | 601 | 4 | US-09-949-016-146136 | Sequence 146136, A |
| 41 | 67 | 3.3 | 601 | 4 | US-09-949-016-146404 | Sequence 146404, A |
| 42 | 66.2 | 3.2 | 601 | 4 | US-09-949-016-156535 | Sequence 156535, A |
| 43 | 66.2 | 3.2 | 231129 | 4 | US-09-949-016-16110 | Sequence 16110, A |
| 44 | 66.2 | 3.2 | 266293 | 4 | US-09-949-016-11934 | Sequence 11934, A |
| 45 | 65.8 | 3.2 | 12313 | 4 | US-09-949-016-13248 | Sequence 13248, A |

ALIGNMENTS

RESULT 1
US-08-911-434A-2
Sequence 2, Application US/08911434A
Patent No. 5959176
GENERAL INFORMATION:
APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 22040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,434A
FILING DATE: 12-AUG-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185-0199P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: DAUCUS CAROTA L.
INDIVIDUAL ISOLATE: KURODA GOSUN
FEATURE:
NAME/KEY: promoter
LOCATION: 1..2042
US-08-911-434A-2
Query Match 11.8%; Score 241.2; DB 2; Length 2042;
Best Local Similarity 72.8%; Pred. No. 5,4e+42;

Matches 367; Conservative 0; Mismatches 128; Indels 9; Gaps 4;

QY 1554 AAATGATATCTGAAAAGCAATATATCTTTGTAAACAGCG---TTGGTCAAAATG 1609

Db 1543 AAATATTTATCTAAAGATTAACATCTTTGTAACAAACCTGGCCAAATAGACCATATA 1602

QY 1610 GGAAGTCATGATGATTCATATAGTTTATATATTAAGTAAATTTTAAATTTATTTATTT 1669

Db 1603 CCAAGTCAGGTGATTTCTAAATGTTAACTAACTAGATGATTTTCTT--TTCAAGGT 1660

QY 1670 TTTGTTTCAGAAATTTAAATTAATATATTTAGGATGGAAGTTCAAGGATCATTTAGGC 1729

Db 1661 ATTAAGTTAATTTCTCAATCAATTAATTAATTTGAGCATTAATGAGCACTTTATGCC 1720

QY 1730 AGCATGACCTGTTTGAACATGATGTCGGGTGATCATTTATGACCTTTCACTCAAC 1789

Db 1721 CAGGTGATTTGTTTAAACAGCTTTGTGCGGATATATTTATTTAGCATTTCAACTCAAGC 1780

QY 1790 TAGTGAAT--ATGCAATCTTGAATATACATCTTTTCAAAATTTCAACAAACAGCTTTACT 1848

Db 1781 TAGCCAGTGAATGCTTTCTAGAAATATATCTTTTGAATTTCAACAAACAGCATTAAT 1840

QY 1849 TTTCTTTCAAGGATTTGAATGCTTTTCTTAACTTTTAAATTAATTAATTAATTTGATTA 1908

Db 1841 TTTCTTTTAAACAGATTTAGATGCTTTCTTAACTTTTAAATTT--AAAAATACATTAAT 1898

QY 1909 GTATATTTTATCAACACTCAACATTTGATTTAGGCTATTAATTTAGTCTTTGATG 1968

Db 1899 ATAAATTTTATCAACACTCAACATTTGATTTAGGCTATTAATTTAGTCTTTGATG 1958

QY 1969 CTCTACTATCATCATCAATCAATTTTACACCAAACTTTAGCTTAATTTTCTTACTTAT 2028

Db 1959 CTCTACTATCATCATCAATCAATTTTACACCAAACTTTAGCTTAATTTTCTTACTTAT 2018

QY 2029 CTCAGCAATACATTTCTAATATATC 2052

Db 2019 TTTAGCAAAACATTTCTAAGGTC 2042

RESULT 2

US-08-911-434A-1

Sequence 1, Application US/08911434A

Patent No. 5859176

GENERAL INFORMATION:

APPLICANT: TORIKAI, Satomi

APPLICANT: OEDA, Kenji

TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: P.O. BOX 747

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22040

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,434A

FILING DATE: 12-AUG-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Raymond C.

REGISTRATION NUMBER: 21,066

REFERENCE/DOCKET NUMBER: 2185-0199P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)205-8000

TELEFAX: (703)205-8050

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Daucus carota L.

INDIVIDUAL ISOLATE: Kuroda Gosun

FEATURE:

NAME/KEY: promoter

LOCATION: 1..247

US-08-911-434A-1

Query Match

Best Local Similarity 9.6%; Score 196.6; DB 2; Length 247;

Matches 223; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 1804 TCTAGAAATACATCTTTTCAATTTCAACAAACAGCTTTACTTTCTTCAACGAT 1863

Db 1 TCTAGAAATATATCTTTTGAATTTCAACAAACAGCATTAATTTCTTTTAAACGAT 60

QY 1864 TGAATCTTTTCTTAACTTTTAAATTAATTAATTAATTAATTAATTTATATCAAC 1923

Db 61 TGAATCTTTTCTTAACTTTTAAATTT--AAAAATACATTAATTAATTTATCAAC 118

QY 1924 ACCTCAGATTTAGTGTGCTACTATTAATTTAGTGTGCTGTGCTCTACTATCAATC 1983

Db 119 ACCTCAGATTTAGTGTGCTACTATTAATTTAGTGTGCTGTGCTCTACTATCAATC 178

QY 1984 ATCATCTTTTCAACCAACCACTTTAGCTTAATTTTCTTACTTATTTCAACATTAAT 2043

Db 179 ATCATCTTTTCAACCAACCACTTTAGCTTAATTTTCTTACTTATTTTGAACAAACAT 238

QY 2044 CTAAATATC 2052

Db 239 CTAAAGGTC 247

RESULT 3

US-09-352-608-2

Sequence 2, Application US/09352608

Patent No. 6218598

GENERAL INFORMATION:

APPLICANT: ISHIGE, Rumiharu

APPLICANT: NISHIKAWA, Satomi

TITLE OF INVENTION: Plant Promoter

FILE REFERENCE: 2185-0353P

CURRENT APPLICATION NUMBER: US/09/352,608

CURRENT FILING DATE: 1999-07-13

EARLIER APPLICATION NUMBER: 10-200372 JAPAN

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 246

TYPE: DNA

ORGANISM: Daucus carota

US-09-352-608-2

Query Match

Best Local Similarity 9.5%; Score 195.6; DB 3; Length 246;

Matches 222; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 1805 TCTAGAAATACATCTTTTCAATTTCAACAAACAGCTTTACTTTCTTCAACGAT 1864

Db 1 TCTAGAAATATATCTTTTGAATTTCAACAAACAGCATTAATTTCTTTTAAACGAT 60

QY 1865 GGAATCTTTTCTTAACTTTTAAATTAATTAATTAATTAATTTATTTATCAAC 1924

Db 61 AGAATCGTTCTTAACTTTTAAATTT--AAAAATACATTAATTAATTTATCAAC 118

| QY | 1985 | TCATCTTACACGCAAAACCTTGAGCTTAATTTTCTACTATTCTCAGCAATTAACATTC | 2045 |
|--|------|--|------|
| QY <td>1985</td> <td> </td> <td> </td> | 1985 | | |
| Db | 179 | TCATCTTTCAGCACAACCTTGAGCTTAATCTTTCTACTAATTTTTCAGAAAAACATTC | 238 |
| QY | 2045 | | |
| Db | 239 | TAAAGTTC | 246 |

```

RESULT 4
US-09-352-608-6
: Sequence 6, Application US/09352608
: Patent No. 6218598
:
GENERAL INFORMATION:
: APPLICANT: ISHIGE, Fumiharu
: APPLICANT: NISHIKAWA, Satomi
: APPLICANT: OEDA, Kenji
: TITLE OF INVENTION: Plant Promoter
: FILE REFERENCE: 2185-0353P
: CURRENT APPLICATION NUMBER: US/09/352, 608
: CURRENT FILING DATE: 1999-07-13
: EARLIER APPLICATION NUMBER: 10-200372 JAPAN
: EARLIER FILING DATE: 1998-07-15
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 140
: TYPE: DNA
:
ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:primer
: US-09-352-608-6

```

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1 RESULT 5
2 US-09-352-608-7/c
3 ; Sequence 7, Application US/09352608
4 ; Patent No. 6218598
5 ; GENERAL INFORMATION:
6 ; APPLICANT: ISHIGE, Fumiharu
7 ; APPLICANT: NISHIKAWA, Satomi
8 ; APPLICANT: OEDA, Kenji
9 ; TITLE OF INVENTION: Plant Promoter
10 ; FILE REFERENCE: 2185-0353P
11 ; CURRENT APPLICATION NUMBER: US/09/352,608
12 ; CURRENT FILING DATE: 1999-07-13
13 ; EARLIER APPLICATION NUMBER: 10-200372 JAPAN
14 ; EARLIER FILING DATE: 1998-07-15
15 ; NUMBER OF SEQ ID NOS: 20
16 ; SOFTWARE: PatentIn Ver. 2.0
17 ; SEQ ID NO 7
18 ; LENGTH: 140
19 ; TYPE: DNA

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; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-352-608-7

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| | | | | |
|-----------------------|-----------------|---|-----------|-------------|
| Query Match | 5.8% | Score 119; | DB 3; | Length 140; |
| Best Local Similarity | 92.6% | Pred. No. 2.8e-16; | | |
| Matches 125; | Conservative 0; | Mismatches 10; | Indels 0; | Gaps 0; |
| QY | 1918 | ATCAACACCTCAACATTGATGTTAGCGCTACTATATAATAGTGCTCTTGCGCTCTACTAT | 1977 | |
| Db | 140 | ATCAACACCTCAACATTGATGTTAGCGCTACTATATAATAGTGCTCTTGCGCTCTACTAT | 81 | |
| QY | 1978 | CATCAACATCAATCTTACACCAACCAACTTGAGCTTAATTTTCTACTTATTTCTAGCAAT | 2037 | |
| Db | 80 | CATCAACATCAATCTTACACCAACCAACTTGAGCTTAATTTTCTACTTATTTTCTAGCAAA | 21 | |
| QY | 2038 | AACATTTCTAATATATC | 2052 | |
| Db | 20 | AACATTTCTAAGGTC | 6 | |

```

RESULT 6
US-09-949-016-12776
; Sequence 12776, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12776
; LENGTH: 187169
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) _ (187169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776

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| | Query Match | Best Local Similarity | 4.0% ; Score 81.4 ; DB 4 ; Length 187169 ; |
|----|--|-----------------------|--|
| | Matches | 41% ; Conservative | 0 ; Mismatches 496 ; Indels 8 ; Gaps 3 ; |
| QY | 883 ATTTCTTAAAGTAATGTAAACTGATCTAAGCACATAGAATTAGTACAGGTTAAAA | 942 | |
| Db | 465 ATATATATATAAAAATATATAATATATATATATATATATATATATATATATATATAT | 524 | |
| QY | 943 CTTTACAAGAATTATATATATTAAGCAAAATCATTTTAACATGTCCTCGGCTGCATT | 1002 | |
| Db | 525 ATATATATATATAAT | 584 | |
| QY | 1003 ATAATAGGATCATCTATGATCATCCATTAAAACTGTTAAAACAAATTCAATGAGAT | 1062 | |
| Db | 585 TAATATATATATCTAT | 644 | |
| QY | 1063 AAAATATCTTACATGAATGAAAAAGAGCAATGTCCTTGAAAAACAAATNGGTATCCC | 1122 | |
| Db | 645 AT | 704 | |
| QY | 1123 TCCGTCCTCTGAATGTATATACATATGATTGGACACGAGACTAGAAAAATGTATPAA | 1182 | |

US-09-949-016-15851
 / Sequence 15851, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / PRIOR FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FaSeq for Windows Version 4.0
 / SEQ ID NO 15851
 / LENGTH: 205044
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc.feature
 / LOCATION: (1)...(205044)
 / OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-15851

Query Match 3.5%; Score 72.2; DB 4; Length 205044;
 Best Local Similarity 48.0%; Pred. No. 1.3e-05;
 Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

QY 1135 AATGATCATATGATTTGGACGAGACTAAGAAATGTAAGTAAGTGAAGT 1194
 DB 200520 ATATATTTATATATTTTAAATATATATATATATATATATTTTAAAT 200579
 QY 1195 AAAAAAGAGAGAAAGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1250
 DB 200580 ATAAAT 200639
 QY 1251 ATGATTTAGAAAAGTAGTTGAAAGTAGTGGGTGGGTGGGTGGGTGGGT 1310
 DB 200640 ATATATTTTAAATATATATATATATATATATATATATATATATATAT 200699
 QY 1311 TACTATTTTGAGAAAGTTTGAATGTATATGATGAGGAGCATCCATTAAG 1370
 DB 200700 AAT 200759
 QY 1371 TGTATGAAATTAAGTGAAGGAGGAGTAATACCTTTATGATATATATAT 1430
 DB 200760 TATTAAT 200819
 QY 1431 TTGATTTGATTAAGTATATATATATATATATATATATATATATATATAT 1490
 DB 200820 TTTTAAAT 200879
 QY 1491 TATATTAATTCGATTAAGTCGATTAACCGCTTTATATATTTTACATCTG 1550
 DB 200880 TATTTTAAATATATATATATATATATATATATATATATATATATAT 200939
 QY 1551 AATTAATCGATTATCGAAGCAATATATCTTTGTAAGACAGCGTTCGCTCA 1606
 DB 200940 TATATTTTAAATATATATATATATATATATATATATATATATATAT 200999
 QY 1607 -----ATGGAAGTTCATGTATTCATATAGTTTAAATATTAAGTAA 1661
 DB 201000 TATATATTTTAAATATATATATATATATATATATATATATATATAT 201059
 QY 1662 TTGTTATTTTGGTTTCAGAAATTTAAATTAATTTATGA 1700
 DB 201060 TATATATATTTTAAATATATATATATATATATATATATATATAT 201098

RESULT 9
 US-09-949-016-15852
 / Sequence 15852, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / PRIOR FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FaSeq for Windows Version 4.0
 / SEQ ID NO 15852
 / LENGTH: 205044
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc.feature
 / LOCATION: (1)...(205044)
 / OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-15852

Query Match 3.5%; Score 72.2; DB 4; Length 205044;
 Best Local Similarity 48.0%; Pred. No. 1.3e-05;
 Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

QY 1135 AATGATCATATGATTTGGACGAGACTAAGAAATGTAAGTAAGTGAAGT 1194
 DB 200520 ATATATTTTATATATTTTAAATATATATATATATATATATTTTAAAT 200579
 QY 1195 AAAAAAGAGAGAAAGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1250
 DB 200580 ATAAAT 200639
 QY 1251 ATGATTTAGAAAAGTAGTTGAAAGTAGTGGGTGGGTGGGTGGGTGGGT 1310
 DB 200640 ATATATTTTAAATATATATATATATATATATATATATATATATATAT 200699
 QY 1311 TACTATTTTGAGAAAGTTTGAATGTATATGATGAGGAGCATCCATTAAG 1370
 DB 200700 AAT 200759
 QY 1371 TGTATGAAATTAAGTGAAGGAGGAGTAATACCTTTATGATATATATAT 1430
 DB 200760 TATTAAT 200819
 QY 1431 TTGATTTGATTAAGTATATATATATATATATATATATATATATATATAT 1490
 DB 200820 TTTTAAAT 200879
 QY 1491 TATATTAATTCGATTAAGTCGATTAACCGCTTTATATATTTTACATCTG 1550
 DB 200880 TATTTTAAATATATATATATATATATATATATATATATATATATAT 200939
 QY 1551 AATTAATCGATTATCGAAGCAATATATCTTTGTAAGACAGCGTTCGCTCA 1606
 DB 200940 TATATTTTAAATATATATATATATATATATATATATATATATATAT 200999
 QY 1607 -----ATGGAAGTTCATGTATTCATATAGTTTAAATATTAAGTAA 1661
 DB 201000 TATATATTTTAAATATATATATATATATATATATATATATATATAT 201059
 QY 1662 TTGTTATTTTGGTTTCAGAAATTTAAATTAATTTATGA 1700
 DB 201060 TATATATATTTTAAATATATATATATATATATATATATATATAT 201098

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RESULT 10
US-09-949-016-15853
; Sequence 15853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15853
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15853
```

```
Query Match 3.5%; Score 72.2; DB 4; Length 205044;
Best Local Similarity 48.0%; Pred. No. 1.3e-05;
Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

Qy 1135 AAATGTATACATATGATTTGGACACGAGCTAAGAAAATGRTAAAGTAACTAGT 1194
Db 200520 ATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 200579
Qy 1195 AAAAAGAAAGAAAGAAAGTGGTAAAGTACGGGACCCACCAATATATATA---TTG 1250
Db 200580 ATAAATATATATATATATATATATATATATATATATATATATATATATAT 200639
Qy 1251 ATGATTTAGAAAAGTGTGAAGTGTGGTGGTGGGATTTTATATATATATATAT 1310
Db 200640 ATATATTTTAAATATATATATATATATATATATATATATATATATATATAT 200699
Qy 1311 TACTATTTTGAGAAAGTTTGAATGATATGAAATGTGGGACCATCTAAAGAAAG 1370
Db 200700 AAATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 200759
Qy 1371 TGTATAGATTTAAATGGGACAGAGGAGTAACTCTTATGATATATATATATAT 1430
Db 200760 TATTAATATATATATATATATATATATATATATATATATATATATATAT 200819
Qy 1431 TTGATTTTCAATAGATTAATATCTATGTTATATATATATATATATATATATAT 1490
Db 200820 TTTTAAATATATATATATATATATATATATATATATATATATATATATAT 200879
Qy 1491 TATATTAATTCGATTAAGTATGATTAACGCTTTTATATATTTTAAACATATCT 1550
Db 200880 TATTTTAAATATATATATATATATATATATATATATATATATATATATAT 200939
Qy 1551 AATTAATCGATTTTCGAAAGCAATATATCTTTGTAACAGCGTTCGGTCAA--- 1606
Db 200940 TATATTTTAAATATATATATATATATATATATATATATATATATATATAT 200999
Qy 1607 -----ATGGAAGTTCAGTGTATCAATAGTTTAAATATATATATATATAT 1661
Db 201000 TATATATTTTAAATATATATATATATATATATATATATATATATATATAT 201059
Qy 1662 TTGTTATTTTGTTCAGAAATTTAAATTAATTAATTAATTAATTAATTAATTA 1700
Db 201060 TATATATATTTTAAATATATATATATATATATATATATATATATATATAT 201098
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RESULT 11
US-09-949-016-12387
; Sequence 12387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12387
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12387
```

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Query Match 3.5%; Score 72.2; DB 4; Length 223471;
Best Local Similarity 48.0%; Pred. No. 1.3e-05;
Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

Qy 1135 AAATGTATACATATGATTTGGACACGAGCTAAGAAAATGRTAAAGTAACTAGT 1194
Db 170947 ATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 171006
Qy 1195 AAAAAGAAAGAAAGAAAGTGGTAAAGTACGGGACCCACCAATATATATA---TTG 1250
Db 171007 ATAAATATATATATATATATATATATATATATATATATATATATATATAT 171066
Qy 1251 ATGATTTAGAAAAGTGTGAAGTGTGGTGGTGGGATTTTATATATATATATAT 1310
Db 171067 ATATATTTTAAATATATATATATATATATATATATATATATATATATATAT 171126
Qy 1311 TACTATTTTGAGAAAGTTTGAATGATATGAAATGTGGGACATCATTAAGAAAG 1370
Db 171127 AAATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 171186
Qy 1371 TGTATAGATTTAAATGGGACAGAGGAGTAACTCTTATGATATATATATATAT 1430
Db 171187 TATTAATATATATATATATATATATATATATATATATATATATATATAT 171246
Qy 1431 TTGATTTTCAATAGATTAATATCTATGTTATATATATATATATATATATATAT 1490
Db 171247 TTTTAAATATATATATATATATATATATATATATATATATATATATATATAT 171306
Qy 1491 TATATTAATTCGATTAAGTATGATTAACGCTTTTATATATTTTAAACATATCT 1550
Db 171307 TATTTTAAATATATATATATATATATATATATATATATATATATATATATAT 171366
Qy 1551 AATTAATCGATTTTCGAAAGCAATATATCTTTGTAACAGCGTTCGGTCAA--- 1606
Db 171367 TATATTTTAAATATATATATATATATATATATATATATATATATATATATAT 171426
Qy 1607 -----ATGGAAGTTCAGTGTATCAATAGTTTAAATATATATATATATAT 1661
Db 171427 TATATATTTTAAATATATATATATATATATATATATATATATATATATAT 171486
Qy 1662 TTGTTATTTTGTTCAGAAATTTAAATTAATTAATTAATTAATTAATTAATTA 1700
```

Db 171487 TATATATATTAAATATATATATATATATATATTTA 171525

RESULT 12

US-09-949-016-12724
; Sequence 12724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12724
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724

Query Match 3.5%; Score 72.2; DB 4; Length 223471;

Best Local Similarity 48.0%; Pred.No.1.3e-05;

Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

Db 1135 AATGATATCATATGATTTGACACGAGACTAAGAAAAATGATTAAGTATGAGT 1194
170947 ATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 171006
QY 1195 AAAAAAG 1250
171007 ATAAAT 171066
Db 1251 ATATGATTTGAG 1310
171067 ATATATTTTAAATATATATATATATATATATATATATATATATATATAT 171126
QY 1311 TACTATTTTGAAG 1370
171127 AATATATTTAT 171186
Db 1371 TGTATGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
171187 TATTAAT 171246
QY 1431 TTGATTTGATTAAGATTAATATATATATATATATATATATATATATATAT 1490
171247 TTTTAAAT 171306
Db 1491 TATATATATTTGATTAAGATTAATATATATATATATATATATATATATAT 1550
171307 TATTTTAAAT 171366
QY 1551 AATTAATCATATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
171367 TATATTTTAAAT 171426
Db 1607 -----ATGGAGAGTTCATGTGATTCATATAGTTTAAATATATATATAT 1661
171427 TATATTTTAAAT 171486
QY 1662 TTGTTATTTTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1700

Db 171487 TATATATATTAAATATATATATATATATATATTTA 171525

RESULT 13

US-09-949-016-12725
; Sequence 12725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12725
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725

Query Match 3.5%; Score 72.2; DB 4; Length 223471;

Best Local Similarity 48.0%; Pred.No.1.3e-05;

Matches 278; Conservative 0; Mismatches 288; Indels 13; Gaps 2;

Db 1135 AATGATATCATATGATTTGACACGAGACTAAGAAAAATGATTAAGTATGAGT 1194
170947 ATATATTTATATATATTTTAAATATATATATATATATATATATATATAT 171006
QY 1195 AAAAAAG 1250
171007 ATAAAT 171066
Db 1251 ATATGATTTGAG 1310
171067 ATATATTTTAAATATATATATATATATATATATATATATATATATATAT 171126
QY 1311 TACTATTTTGAAG 1370
171127 AATATATTTAT 171186
Db 1371 TGTATGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
171187 TATTAAT 171246
QY 1431 TTGATTTGATTAAGATTAATATATATATATATATATATATATATATATAT 1490
171247 TTTTAAAT 171306
Db 1491 TATATATATTTGATTAAGATTAATATATATATATATATATATATATATAT 1550
171307 TATTTTAAAT 171366
QY 1551 AATTAATCATATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
171367 TATATTTTAAAT 171426
Db 1607 -----ATGGAGAGTTCATGTGATTCATATAGTTTAAATATATATATAT 1661
171427 TATATTTTAAAT 171486
QY 171427 TATATTTTAAAT 171486

| | | | | | | | |
|----|--------|------------|----------|---------|----------|----------|--------|
| QY | 1662 | TTGTTATTTT | GTTCAGAA | TTTAAAT | TAAATTAT | TGGA | 1700 |
| | | | | | | | |
| Db | 171487 | TATATATATT | TAAATAT | TAAATAT | AAAAATAT | ATATTTTA | 171525 |

RESULT 14

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US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
;
; GENERAL INFORMATION:
;
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLPX VIRUS
; NUMBER OF SEQUENCES: 52
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
;
; COUNTRY: USA
; ZIP: 22313-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMWU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
;
; TELEX: 899149
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F15
;
; US-08-232-463-14

```

Query Match 3.4%; Score 69.4; DB 1; Length 7218;
Best Local Similarity 4.6%; Pred. No. 2.4e-05;
Matches 16; Conservative 212; Mismatches 123; Indels 0; Gaps 0;

| | | | |
|----|------|--|------|
| QY | 105 | ATTGCATGAGTAAAAATCTTACATGAAAGAAAGACATCTCTTTGAAAAACA | 1110 |
| | | | |
| Db | 1461 | ATTTAAAGAGTAAAGAAATTGGTACRRRRRRRRRRRRRRRRRRRRRRRR | 1402 |
| | | | |
| QY | 1111 | ATAGGTACTCCCTCCGCTCCTGAAATGTATCATGTGATGACAGGAGACTAAGA | 1170 |
| | | | |
| Db | 1401 | RR | 1342 |
| | | | |
| QY | 1171 | AAATGTATAAAGTAGTAGAGTAAAGAAAGAAAGAAAGAAAGTGCTAAAGTCGG | 1230 |
| | | | |
| Db | 1341 | RR | 1282 |
| | | | |
| QY | 1231 | GACCCACCAATATATATGATGATGATGAAAAAGTATTGAAAGTAGTGGGTGGTGGG | 1290 |
| | | | |
| | 1291 | RR | 1222 |
| | | | |

```
OY      1201 AATTTTAAATATAAAAAATTACTGATTTTGAAAGAGTTTGAAATGTATGAATTTGGTG 1350
Db      1221 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1162
OY      1351 GGAACATCATTAAGAAGAAATGTATAGAAATTTAAATGGACAAGAGGAGTAA 1401
Db      1161 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1111
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RESULT 15

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US-09-806-708B-22/c
: Sequence 22, Application US/09806708B
: Patent No. 6784342
: GENERAL INFORMATION:
: APPLICANT: The University of British Columbia
: TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
: FILE REFERENCE: 4810-58741
: CURRENT APPLICATION NUMBER: US/09/806,708B
: PRIOR FILING DATE: 2001-04-03
: PRIOR APPLICATION NUMBER: US 60/147,133
: PRIOR FILING DATE: 1999-08-04
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (1)..(1141)
: OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEI promoters
US-09-806-708B-22

```

| | | | | |
|-----------------------|-------------------|--------------------|------------|--------------|
| Query Match | 3.3%; | Score 68.6; | DB 4; | Length 1141; |
| Best Local Similarity | 13.1%; | Pred. No. 2.4e-05; | | |
| Matches 141; | Conservative 392; | Mismatches 536; | Indels 10; | Gaps 5; |

[illegible]

